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192545

m9

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From: Vogel, Nancy
Sent: Monday, June 12, 2006 9:13 AM
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Subject: sequence search 09/896,888

please do a sequence search, including interference files, of

SEQ ID NO:1 (entire),
bp. 351-527 of SEQ ID NO: 1,

of 09/896888, and return results to me on paper asap.

Thanks
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Searcher: _____
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Date Searcher Picked up: _____
Date completed: _____
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Type of Search
NA# _____ AA# _____
S/L: _____ Oligomer: _____
Encode/Transl: _____
Structure #: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable
STN: _____
DIALOG: _____
QUESTEL/ORBIS: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
WWW/Internet: _____
Other (Specify): _____

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RESULT 2
NPHTTA 4170 bp DNA linear VRL 02-AUG-1993
LOCUS Orygia pseudotsugata nuclear polyhedrosis virus transcriptional
DEFINITION trans-activator (IE-2) gene, complete cds; ORF, complete cds.
ACCESSION M83827
VERSION M83827.1 GI:332540
KEYWORDS transcriptional transactivator.
SOURCE Orygia pseudotsugata single capsid nucleopolyhedrovirus
ORGANISM Orygia pseudotsugata single capsid nucleopolyhedrovirus
          Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
          Nucleopolyhedrovirus.
REFERENCE 1 (bases 1 to 4170)
AUTHORS Theilmann,D.A. and Stewart,S.
TITLE Molecular analysis of the trans-activating IE-2 gene of Orygia
JOURNAL pseudotsugata multicapsid nuclear polyhedrosis virus
PUBMED Virolology 187 (1), 84-96 (1992)
1736546
REFERENCE 2 (bases 1 to 4170)
AUTHORS Theilmann,D.A. and Stewart,S.
TITLE Tandemly repeated sequence at the 3' end of the IE-2 gene of the
JOURNAL baculovirus Orygia pseudotsugata multicapsid nuclear polyhedrosis
PUBMED virology 187 (1), 97-106 (1992)
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RESULT 3
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 LOCUS Orygia pseudotsugata multicapsid nucleopolyhedrovirus, complete
 DEFINITION genome.
 ACCESSION U75930
 VERSION U75930.2 GI:11024985
 KEYWORDS Orygia pseudotsugata MNPV
 SOURCE Orygia pseudotsugata MNPV
 ORGANISM Viruses; dsDNA viruses, no RNA stage; Baculoviridae; Nucleopolyhedrovirus.

REFERENCE 1 (bases 1 to 131995)
 AUTHORS Ahrens,C.H., Russell,R.L., Funk,C.J., Evans,J.T., Harwood,S.H. and Rohmann,G.F.
 TITLE The sequence of the Orygia pseudotsugata multineocapsid nuclear polyhedrosis virus genome
 JOURNAL Virology 229 (2), 381-399 (1997)
 REFERENCE 2 (bases 1 to 131995)
 AUTHORS Rohmann,G.F.
 TITLE Direct Submission
 JOURNAL Submitted (23-OCT-1996) Oregon State University, Agricultural
 REFERENCE 3 (bases 1 to 131995)
 AUTHORS Rohmann,G.F.
 TITLE Direct Submission
 JOURNAL Submitted (06-MAR-1998) Oregon State University, Agricultural
 REFERENCE 4 (bases 1 to 131995)
 AUTHORS Rohmann,G.F.
 TITLE Sequence update by submitter
 JOURNAL Submitted (26-OCT-2000) Oregon State University, Agricultural
 REMARK COMMENT Sequence update by submitter
 FEATURES On Oct 26, 2000 this sequence version replaced gi:2934903.
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DPDIRADGMYHKECVLTVMHLVACGAPAGSATRLDAVAKIIPNDEGNCAPALAA
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Matches 564; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db	128652	GTCGCCCTTATCGCGCTTAAATATACAGCCGCAACGATCTGTAAACACAGTTGAACG	128711
QY	541	CATCTGTTACAGGACCAACATG 564	
Db	128712	CATCTGTTACAGGACCAACATG 128735	
RESULT 4			
S64501/C			
LOCUS			
DEFINITION			
ACCESSION			
VERSION			
KEYWORDS			
SOURCE			
ORGANISM			
REFERENCE			
TITLES			
AUTHORS			
JOURNAL			
PUBMED			
REMARK			
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gene			

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Query Match 99.7%; Score 562.4; DB 10; Length 1429;
 Best Local Similarity 99.8%; Pred. No. 8.2e-185;
 Matches 563; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CATGATGATTAACAATGATGCTAATGTTGCTTCAACAACAATCTGTTGAACGTG 60
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 DB 765 CATGATGATTAACAATGATGCTAATGTTGCTTCAACAACAATCTGTTGAACGTG 706
 QY |||||
 QY 61 TTTTCATGTTTGCACACAGCCTTTATATCTCGTGCGCTCCCAACCACTTTT 120
 DB |||||
 DB 705 TTTTCATGTTTGCACACAGCCTTTATATCTCGTGCGCTCCCAACCACTTTT 646
 QY |||||
 QY 121 GCACGTGCAAAAACAGCCTTTTGACGCGGCGCCATACATAGTACAACTTACGTTTC 180
 DB |||||
 DB 645 GCACGTGCAAAAACAGCCTTTTGACGCGGCGCCATACATAGTACAACTTACGTTTC 586
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 QY 181 GTAGACATTTTACATAATAGTCTACACGCTGTATACGCTCCAAATACACTACACAC 240
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 DB 585 GTAGACATTTTACATAATAGTCTACACGCTGTATACGCTCCAAATACACTACACAC 526
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 QY 241 ATTGAACCTTTTTCAGTGCACAAAAAGTACGTGTCGACAGTACAGTACGCGGCTTATC 300
 DB |||||
 DB 525 ATTGAACCTTTTTCAGTGCACAAAAAGTACGTGTCGACAGTACAGTACGCGGCTTATC 466
 QY |||||
 QY 301 GGGTCGCGTCTGTACGTAAGTATCACTTATGACCGACGAGTGTGTTTATCGT 360
 DB |||||
 DB 465 GGGTCGCGTCTGTACGTAAGTATCACTTATGACCGACGAGTGTGTTTATCGT 406
 QY |||||
 QY 361 GACAGAGCGCAGCTTCTGTGTTGCTAACCGCAGCGGACGCACTCTTATCGGAACA 420
 DB |||||
 DB 405 GACAGAGCGCAGCTTCTGTGTTGCTAACCGCAGCGGACGCACTCTTATCGGAACA 346
 QY |||||
 QY 421 GAGCGCGCTTCATATCAGCGCGCGCTTATCTCATGCGCGTGAACGAGACGAGCGCCC 480
 DB |||||
 DB 345 GAGCGCGCTTCATATCAGCGCGCGCTTATCTCATGCGCGTGAACGAGACGAGCGCCC 286
 QY |||||
 QY 481 GTCCCGCTTATCGCGCTTATTAATATACGCGCGCAACGATCTGTAAACAGATTGAACAG 540
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 DB 285 GTCCCGCTTATCGCGCTTATTAATATACGCGCGCAACGATCTGTAAACAGATTGAACAG 226
 QY |||||
 QY 541 CATCTGTTACAGAGCAACACATG 564
 DB |||||
 DB 225 CATCTGTTACAGAGCAACACATG 202

RESULT 5
 LOCUS DD212689 2773 bp DNA linear PART 19-JAN-2006
 DEFINITION NOVEL IMMUNOGENIC MIMETICS OF MULTIMER PROTEINS.
 ACCESSION DD212689
 VERSION DD212689.1 GI:85632167
 KEYWORDS JP 2005518194-A/17.
 SOURCE synthetic construct
 ORGANISM synthetic construct

REFERENCE
 1 (bases 1 to 2773)
 Moutilsen,S., Voldborg,B., Bratt,T., Nielsen,F.S. and Klysemer,S.
 NOVEL IMMUNOGENIC MIMETICS OF MULTIMER PROTEINS
 Patent: JP 2005518194-A 17 23-JUN-2005;

COMMENT
 OS Artificial sequence
 PN JP 2005518194-A/17
 PD 23-JUN-2005

PF 15-NOV-2002 JP 2003544079
 PR 16-NOV-2001 DK PA200101702.16-NOV-2001 US 60/331575 PT
 soren moutilsen,bjoern voldborg,tomas bratt,finn scausholm PT
 nielsen,
 PI steen klysemer
 CC p220p2f expression vector for insect cells
 FH Key Location/Qualifiers
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 FT misc_recomb (573)..(578)
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 FT /note='BamHI site'
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ORIGIN

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 Matches 548; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 DB 5 CATGATGATTAACAATGATGCTAATGTTGCTTCAACAACAATCTGTTGAACGTG 64
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 DB 125 GCACGTGCAAAAACAGCCTTTTGACGCGGCGCCATACATAGTACAACTTACGTTTC 184
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 DB 305 GGGTCGCGTCTGTACGTAAGTATCACTTATGACCGACGAGTGTGTTTATCGT 364
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 QY 421 GAGCGCGCTTCATATCAGCGCGCGCTTATCTCATGCGCGTGAACGAGACGAGCGCCC 480
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Qy 481 GTCCCGTTATCGCGCTATTAATACAGCCCGCAACGATCTGTAAACAGATTGAACAG 540
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Db 545 CATCTGTT 552

RESULT 6
AX766573 2773 bp DNA linear PAT 25-JUN-2003
LOCUS Sequence 60 from Patent WO03042244.
ACCESSION AX766573
VERSION AX766573.1 GI:32260450
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 Klysnier, S., Nielsen, F. S., Bratt, T., Voldborg, B. and Mouritsen, S.
AUTHORS Novel immunogenic mimetics of multimer proteins
TITLE Patent: WO 03042244-A 60 22-MAY-2003;
JOURNAL Pharmexa A/S (DK) ; Klysnier, Steen (DK) ; Nielsen, Finn Stenusholm
(DK) ; Bratt, Tomas (DK) ; Voldborg, Bjorn (DK) ; Mouritsen, Soren
(DK)

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ORIGIN
Query Match 97.2%; Score 548; DB 2; Length 2773;
Best Local Similarity 100.0%; Pred. No. 9,4e-180;
Matches 548; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CATTGATGATTAACAAATGATGCTATGCTTGAACAAATCTGTGAACGCTG 60
Db 5 CATTGATGATTAACAAATGATGCTATGCTTGAACAAATCTGTGAACGCTG 64
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Db 65 TTTTCATGTTGGCAACAGACCTTATATCTCGTGGCCCTCCCAACCAACTTTT 124
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Db 125 GCACGTCAAAAAAAGACGCTTTTGACGCGGGCCCATACATAGTACAACCTTAAGTTTC 184
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Db 425 GGACGCGCTCCATATCAGCGCGCGCTTATCTCATGCGGTGACCGGACGAGCGGCC 484
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Db 485 GTCCCGTTATCGCGCTTATTAATACAGCCCGCAACGATCTGTGAACAGATTGAACAG 544
Qy 541 CATCTGTT 548
Db 545 CATCTGTT 552

RESULT 7
AB175497/c 2284 bp DNA linear VRL 29-MAR-2005
LOCUS AB175497/c
DEFINITION Hyphantria cunea nucleopolyhedrovirus ie2, hycu-ep32, odv-ε56 gene
for immediate early gene 2, early protein 32, occlusion derived
virus envelope protein 56, partial and complete cde.
ACCESSION AB175497
VERSION AB175497.1 GI:62086138
KEYWORDS
SOURCE Hyphantria cunea nucleopolyhedrovirus
ORGANISM Hyphantria cunea nucleopolyhedrovirus
Virus; dsDNA viruses, no RNA stage; Baculoviridae;
Nucleopolyhedrovirus.
REFERENCE
1 Shirata, N., Ikeda, M. and Kobayashi, M.
AUTHORS Hyphantria cunea nucleopolyhedrovirus (NPV) ep32 gene is involved
in the restriction of Bombyx mori NPV replication in B. mori cells
JOURNAL Unpublished
TITLE 2 (bases 1 to 2284)
REFERENCE Shirata, N., Ikeda, M. and Kobayashi, M.
AUTHORS Direct Submission
JOURNAL Submitted (26-MAR-2004) Michihiro Kobayashi, Nagoya University,
Graduate School of Bioagricultural Sciences, Laboratory of
Biodynamics, Chikusa, Nagoya, Aichi, 464-8601, Japan
(E-mail: michihiro@agr.nagoya-u.ac.jp, Tel: 81-52-789-4038,
Fax: 81-52-789-4038)

FEATURES
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ORIGIN

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Query Match      24.5%; Score 138.4; DB 10; Length 2284;
Best Local Similarity 78.3%; Pred. No. 2.5e-36;
Matches 166; Conservative 0; Mismatches 46; Indels 0; Gaps 0;

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QY 81 CACCTTATCTCGTGCCCTCCACCACCAACTTTTTCGATCGCAAAAAACAGCT 140
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DB 686 CACCGCTTAATCTGCTGTGACACAGAACTTTTTCGAGTGCAAAAAACAGCTT 627
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QY 141 TTTCGACGCGGCGCCATACATAGTACAACTCTAGTTTTCGTAATTTTTCATTAAT 200
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DB 626 ATGAACACAGCCCCATATACAGAGCAAAAGCTATCTATTGTAATTTTCTTAAT 567
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QY 201 AGCTTACACCGTTGTATACGCTCCAAATACATACACACATTGAACCTTTTTCAGTGC 260
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DB 566 AGCTTACACGTTCTTATACGCTCTTAATACACCTACACAGAGTAACTTTTTCAGAGTGC 507
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QY 261 AAAAAGTAGCTGTGCGGACGTACAGTAGGCGG 292
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DB 506 AAAAATACGTGTGAGAGTACAGTACTCGG 475
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RESULT 8
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DEFINITION      Hyphantria cunea nucleopolyhedrovirus genomic DNA, complete genome.
ACCESSION      AP009046
VERSION      AP009046.1 GI:86198125
KEYWORDS
SOURCE
  Hyphantria cunea nucleopolyhedrovirus
  Hyphantria cunea nucleopolyhedrovirus
  Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
  Nucleopolyhedrovirus.

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REFERENCE
AUTHORS      Felipealves,C.A., Ikeda,M. and Kobayashi,M.
TITLE      Identification and characterization of Hyphantria cunea
            nucleopolyhedrovirus homologous repeated regions
JOURNAL      Virus Gene 25, 281-290 (2002)
AUTHORS      Ikeda,M., Yanagimoto,K. and Kobayashi,M.
TITLE      Identification and functional analysis of Hyphantria cunea
            nucleopolyhedrovirus lap genes
JOURNAL      Virology 321 (2), 359-371 (2004)
PUBMED      15051395
REFERENCE
AUTHORS      Ikeda,M., Shikata,M., Shirata,N., Chaeychomari,S. and Kobayashi,M.
TITLE      Gene organization and sequencing of the Hyphantria cunea

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JOURNAL      unpublished
REFERENCE      4 (bases 1 to 132959)
AUTHORS      Ikeda,M. and Kobayashi,M.
TITLE      Direct Submission
JOURNAL      Submitted (17-AUG-2005) Motozo Ikeda, Nagoya University, Graduate
            School of Biological Sciences, Chikusa, Nagoya, Aichi
            464-8601, Japan (E-mail:mochikoeag@nagoya-u.ac.jp,
            tel:81-52-789-4038, fax:81-52-789-4036)
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Query Match 24.5%; Score 138.4; DB 10; Length 132959;
Best Local Similarity 78.3%; Pred. No. 3,3e-36;
Matches 166; Conservative 0; Mismatches 46; Indels 0; Gaps 0;

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Qy	201	AGCTCACCGCTGTATAGCTCCAAATACATACACACATGAACCTTTTGCAGTGC	260
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RESULT 9
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LOCUS DEFINITION Epiphyas postvittana nucleopolyhedrovirus, complete genome.
ACCESSION AY043265
VERSION AY043265.1 GI:15213125
KEYWORDS
SOURCE Epiphyas postvittana NPV
ORGANISM Epiphyas postvittana NPV
Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
Nucleopolyhedrovirus.
REFERENCE 1 (bases 1 to 118584)
Hynk,O., Dellow,R.A., Olsen,M., Caradoc-Davies,K.M.B., Drake,K.
and Ward,V.K.
TITLE The complete sequence of the Epiphyas postvittana
nucleopolyhedrovirus genome
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 118584)
Hynk,O., Dellow,R.A., Olsen,M., Caradoc-Davies,K.M.B., Drake,K.
and Ward,V.K.

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TITLE      Direct Submission
JOURNAL    Submitted (03-JUL-2001) Microbiology, University of Otago, PO Box
           56, Dunedin, New Zealand
FEATURES   Location/Qualifiers
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[illegible]

FEATURES	source
JOURNAL	Comparative analysis of the genomes of <i>Rachiplusia</i> ou and <i>Autographa californica</i> multiple nucleopolydovirus
PUBLISHED	J. Gen. Virol. 84 (Pt 7), 1827-1842 (2003)
REFERENCES	3 (bases 1 to 131526)
AUTHORS	Bonning, B.C. and Harrison, R.L.
JOURNAL	Submitted (28-AUG-2002) Entomology, Iowa State University, Ames, Iowa 50011, USA
FEATURES	Location/Qualifiers
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CDS
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Best Local Similarity 77.0%; Pred. No. 2..2e-23;
Matches 124; Conservative 0; Mismatches 37; Indels 0; Gaps 0;
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Db 130001 AACTTTTTCAGTGGAAAAAAGTCTTTTCTGCGCATTTCAATATACATACAACT 129942
QY 172 CTACGTTTGTAGACTATTATTACATAATAGTCTACACCGTTGTATACGTCCTCAATACA 231
Db 129941 CTACAAATGGTAGACATTTTATTAGATAGTCTACACGTACATACGCTCCCAATATA 129882
QY 232 CTACCAACATTTGACCTTTTTCAGTGGAAAAAGTACGT 272
Db 129881 CTACTACACTATCAACTTTTTCAGTACAAAAAGTTCAT 129841

RESULT 11
NPHE38/c
LOCUS NPHE38 1511 bp DNA linear VRL 02-AUG-1993
DEFINITION Autographa californica nuclear polyhedrosis virus major early
protein (PE-38) gene, complete cds.
ACCESSION M62488
VERSION M62488
KEYWORDS major early protein PE-38.
SOURCE Autographa californica nucleopolyhedrovirus
ORGANISM Autographa californica nucleopolyhedrovirus
Virus; dsDNA viruses, no RNA stage; Baculoviridae;
Nucleopolyhedrovirus.
REFERENCE 1 (bases 1 to 1511)
Krapapa R. and Knebel-Morsdorf, D.
Identification of the very early transcribed baculovirus gene PE-38
J. Virol. 65 (2), 805-812 (1991)
PUBMED 1987375
COMMENT Original source text: Autographa californica nuclear polyhedrosis


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/note="BRO: 3769 Da primary translation product"
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repeat_region

gene
CDS

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 4935. .5921
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 Best Local Similarity 80.6%; Pred. No. 9.2e-23;
 Matches 129; Conservative 0; Mismatches 30; Indels 1; Gaps 1;

Qy 112 AACCTTTTGCACGCGAAAAACAGCCTTTTGACGCGGCGCCATACATG-GTACAAAC 170
 Db 125539 AACATTATTCAGAGCAAAAAAGTTCCTTTTATTCGACCCCTATATACATACCAAC 125598

Qy 171 TCTACGTTTGTAGACTATTTTACATTAATAGTCTACACCGTGTATACGCTCAATAAC 230
 Db 125599 TCTACGTTTGTAGACTATTTTAACTGAAATAGTCTACACGTTGTATACGCTCCCAATAC 125658

Qy 231 ACTACCAACATTTGAACCTTTTGCAGTGCAGAAAAAGTAC 270
 Db 125659 ACTACCAACATCGAAGCTTTTGCACCTGCAATTAAGTTTC 125698

RESULT 15
 AY846866/c 1602 bp DNA linear VRL 12-JAN-2005
 LOCUS Antheraea pernyi nucleopolyhedrovirus occlusion-derived virus
 DEFINITION Antheraea-56 protein (odv-e56) gene, complete cds.
 ACCESSION AY846866
 VERSION AY846866.1 GI:57233514
 KEYWORDS Antheraea pernyi nucleopolyhedrovirus
 SOURCE Antheraea pernyi nucleopolyhedrovirus
 ORGANISM Viruses: deDNA viruses, no RNA stage; Baculoviridae;
 Nucleopolyhedrovirus.
 REFERENCE 1 (bases 1 to 1602)
 AUTHORS Xia,A., Li,W., Mu,Z., Li,J., Zhou,Q. and Zhang,Z.
 TITLE Cloning and analysis of occlusion-derived virus envelope-56 gene of
 Antheraea pernyi nuclear polyhedrosis virus
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 1602)
 AUTHORS Xia,A., Li,J., Li,W., Zhou,Q. and Zhang,Z.
 TITLE Direct Submission
 JOURNAL Submitted (04-DEC-2004) Insect Pathology, The Sarcicltural Research
 Institute Caas, Shabaidu, Zhenjiang, Jiangsu 212018, China

FEATURES
 source location/Qualifiers
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ORIGIN
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 Best Local Similarity 82.5%; Pred. No. 2.5e-22;
 Matches 137; Conservative 0; Mismatches 26; Indels 3; Gaps 2;

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Db	116	AGTCTAGCTTTCGTAGCTATTTTACCTAATAGTCTACACTGTCTATAGCTGCCAAT	57
Qy	229	ACACTACC--ACACATTGAACCTTTTGCAGTGCAAAAAGTAGT	272
Db	56	ACACTACCCCTTAAACCAAACTATTTTGCAGTGCAAAAAGTAGCT	11

Search completed: June 15, 2006, 19:57:54
 Job time : 4072.26 secs

GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: June 15, 2006, 16:18:24 ; Search time 603.579 Seconds
(without alignments)
6515.052 Million cell updates/sec

Title: US-09-896-888a-1
Perfect score: 564
Sequence: 1 catgatgataacaatgcatg.....tggtacagcagacacacatg 564

Scoring table: IDENTITY NUC
Gapop 10% , Gapext 1.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 10489840

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_8:*

- 1: geneseqn1980s:*
- 2: geneseqn1990s:*
- 3: geneseqn2000s:*
- 4: geneseqn2001as:*
- 5: geneseqn2001bs:*
- 6: geneseqn2002as:*
- 7: geneseqn2002bs:*
- 8: geneseqn2003as:*
- 9: geneseqn2003bs:*
- 10: geneseqn2003cs:*
- 11: geneseqn2003ds:*
- 12: geneseqn2004as:*
- 13: geneseqn2004bs:*
- 14: geneseqn2005as:*
- 15: geneseqn2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	* Query Match	Length	DB ID	Description
1	564	100.0	564	2	AAV62487
2	548	97.2	560	12	ADQ48575
3	548	97.2	2773	9	AAI61306
4	546.4	96.9	5038	12	ADQ48539
5	101.4	18.0	279	2	AAI13730
6	101.4	18.0	133894	2	AAI13730
7	93.4	16.6	28413	10	ADCS1646
8	62	11.0	141	12	ADQ48576
9	39.6	7.0	6289	8	ABZ10059
10	39.6	7.0	9289	4	AAI46501
11	39.6	7.0	9289	10	ADQ48575
12	38	6.7	9289	8	ABZ10059
13	38	6.7	9289	10	ADQ48575
14	37.4	6.6	2000	11	ACI35887
15	36.2	6.4	2000	8	ADQ48575
16	35.4	6.3	986	6	ABQ68715
17	35.4	6.3	1549	6	ABQ70339
18	34.4	6.1	855	2	AAV34232

19	34.4	6.1	855	8	ACD08103	ACD08103 cDNA enco
20	34.4	6.1	855	14	ADZ12289	Adz12289 Human sec
21	34	6.0	18977	4	ABL19380	ABL19380 Prosopill
22	33.8	6.0	1991	6	AAI18541	AAI18541 Partiel g
23	33.8	6.0	2117	11	ACN44823	ACN44823 Human mRN
24	33.8	6.0	3056	8	ABZ42667	Abz42667 Human gal
25	33.8	6.0	3061	14	ADZ13224	Adz13224 Human can
26	33.8	6.0	3083	2	AAQ97304	AAQ97304 Galanin r
27	33.8	6.0	3203	13	ACN43223	ACN43223 Human dia
28	33.8	6.0	39344	11	ACN44822	ACN44822 Human gen
29	33.8	6.0	40318	14	ADZ13223	Adz13223 Human can
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31	33.2	5.9	43053	8	ABZ73951	Abz73951 Secreted
32	33.2	5.9	43053	10	ABZ67535	Abz67535 Human sec
33	33.2	5.9	43056	8	ABZ73950	Abz73950 Secreted
34	33.2	5.9	43056	10	ABZ67534	Abz67534 Human sec
35	33	5.9	14429	6	ABL34242	ABL34242 Human ang
36	33	5.9	14429	6	ABQ67097	Abq67097 Human imm
37	32.8	5.8	426	3	AAH30400	AAH30400 Human col
38	32.8	5.8	454	6	ABL93815	ABL93815 Arabidops
39	32.8	5.8	1110	3	AAI37066	AAI37066 Arabidops
40	32.8	5.8	1251	3	AAI36504	AAI36504 Arabidops
41	32.8	5.8	2000	6	ABZ17343	Abz17343 Arabidops
42	32.8	5.8	2000	8	ADA68882	Ada68882 Arabidops
43	32.8	5.8	2489	14	ADQ70711	Adq70711 Rice gene
44	32.8	5.8	2780	8	ADA70711	Ada70711 Rice gene
45	32.6	5.8	495	5	ADL37609	ADL37609 Human ova

ALIGNMENTS

RESULT 1	
ID	AAV62487 standard; DNA; 564 BP.
XX	
AC	AAV62487;
XX	
DT	17-OCT-2003 (revised)
DT	19-JAN-1999 (first entry)
XX	
DE	O. pseudotsugata multicapsid nucleopolyhedrosis virus 1e2 promoter.
XX	
KM	Orygia pseudotsugata; multicapsid; nucleopolyhedrosis virus; OpMPV;
KM	Op 1e2; promoter; shuttle vector; transformation; melanotransferin;
KM	Immediate early baculovirus promoter; prokaryotic; transcription;
KM	bleomycin/bleomycin-type antibiotic; insect cell; transposon;
XX	ion transport peptide hormone; ss.
OS	Orygia pseudotsugata; polynhedrosis virus.
XX	
PN	WO9844141-A2.
XX	
PD	08-OCT-1998.
XX	
PF	26-MAR-1998; 98MO-CN000282.
XX	
PR	27-MAR-1997; 97US-0049946P.
PR	28-JAN-1998; 98CA-02221819.
XX	
PA	(UYBR-) UNIV BRITISH COLUMBIA.
XX	
PI	Grigliatti TA, Theilmann DA, Pfeifer TA, Hegedus DD;
XX	
DR	WPI; 1998-557129/47.
XX	
PT	Expression vectors for transforming insect cells from disparate lines -
PT	useful to express heterologous DNA, e.g. to allow study of gene
PT	expression and produce commercially important proteins.
XX	
PS	Claim 10; Page 82; 121pp; English.
XX	
CC	This represents a Orygia pseudotsugata multicapsid nucleopolyhedrosis

CC virus (OpMNPV) immediate early 2 (Op iez2) promoter sequence. The
 CC invention provides a new shuttle vector for transforming insect cells
 CC that comprises: (i) prokaryotic origin of replication; (ii) insect
 CC promoter having homology to, and capable of functioning as, an immediate
 CC early baculovirus promoter; (iii) prokaryotic promoter sequence, and (iv)
 CC selectable marker capable of conferring resistance to a blomycin/
 CC phleomycin-type antibiotic under transcriptional control of (ii) and
 CC (iii). In insect and prokaryotic cells respectively. The vectors can be
 CC used to stably transform (especially insect) cells with heterologous DNA,
 CC useful to allow study of gene expression and direct expression of
 CC heterologous gene products e.g. commercially important proteins. They are
 CC especially useful to allow expression of the heterologous
 CC melanotransferrins, ion transport peptide hormones or biologically active
 CC derivatives in insect cells. They enable transformation of insect cell
 CC lines from disparate species, allowing screening of lines for optimum
 CC post-translational modification of particular proteins. Shuttle vectors
 CC further comprising DNA transposable elements defining a transposon can be
 CC used to optimise heterologous protein expression and facilitate selection
 CC of desired transformants. (Updated on 17-OCT-2003 to standardise OS
 CC field)

CC
 XX Sequence 564 BP, 147 A, 160 C, 116 G, 141 T, 0 U, 0 Other;

Query Match Best Local Similarity 100.0%; Score 564; DB 2; Length 564;

Matches 564; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CATGATGATTAACAATGATATGCTAATGTTGTTCAACAACAATCTGTGAACGTG 60
 DB 1 CATGATGATTAACAATGATATGCTAATGTTGTTCAACAACAATCTGTGAACGTG 60
 QY TTTTCATGTTGGCCAAAGACCTTTATCTCGGTGGCCCTCCCAACCAACTTTT 120
 DB TTTTCATGTTGGCCAAAGACCTTTATCTCGGTGGCCCTCCCAACCAACTTTT 120
 QY 121 GCACTGCAAAAAACACGCTTTTGACCGCGGCCCATACATAGTACAACTGATTTC 180
 DB 121 GCACTGCAAAAAACACGCTTTTGACCGCGGCCCATACATAGTACAACTGATTTC 180
 QY 181 GTAGACTATTTTACATAAATAGTCTACACCGTTTATACGTTCCAAATACATACAC 240
 DB 181 GTAGACTATTTTACATAAATAGTCTACACCGTTTATACGTTCCAAATACATACAC 240
 QY 241 ATTGAACCTTTTTCAGTGCAGTGCATGTCGCGGAGTCACTGATGAGCGGCTTATC 300
 DB 241 ATTGAACCTTTTTCAGTGCAGTGCATGTCGCGGAGTCACTGATGAGCGGCTTATC 300
 QY 301 GGGTCGGCTCTGTCACTGATGATCACTTATGGAACCGGACGAGTGTCTTATCGT 360
 DB 301 GGGTCGGCTCTGTCACTGATGATCACTTATGGAACCGGACGAGTGTCTTATCGT 360
 QY 361 GACAGACGCGCAAGTTCTGTGTTGCTAACCGGACCGGACGCACTCTTATGGAAACA 420
 DB 361 GACAGACGCGCAAGTTCTGTGTTGCTAACCGGACCGGACGCACTCTTATGGAAACA 420
 QY 421 GGAAGCGCTCCATATACGCGCGCTTATCTCATGCGCGTGAACGAGGCGCC 480
 DB 421 GGAAGCGCTCCATATACGCGCGCTTATCTCATGCGCGTGAACGAGGCGCC 480
 QY 481 GTCCCGCTTATCGGCTTATTAATATACGCGCGCAACATCTGTAAACAGTTGAACAG 540
 DB 481 GTCCCGCTTATCGGCTTATTAATATACGCGCGCAACATCTGTAAACAGTTGAACAG 540
 QY 541 CATCTGTTACAGGACCAACATG 564
 DB 541 CATCTGTTACAGGACCAACATG 564

RESULT 2
 ADQ48575
 ID ADQ48575 standard; DNA, 560 BP.
 XX
 AC ADQ48575;

XX
 DT 09-SEP-2004 (first entry)
 XX
 DE OpIE2 promoter DNA sequence.
 XX
 KM viral vector; recombinant site; recombinant virus;
 KM replication-defective particle generation; gene expression inhibition;
 KM gene therapy vector; de; OpIE2 promoter.
 XX
 OS Unidentified.
 XX
 PN WO2004093768-A2.
 XX
 PD 29-JAN-2004.
 XX
 PF 18-JUL-2003; 2003WO-US022437.
 XX
 PR 18-JUL-2002; 2002US-0396335P.
 PR 26-JUL-2002; 2002US-0398617P.
 PR 19-NOV-2002; 2002US-0427231P.
 PR 24-MAR-2003; 2003US-0456496P.
 PR 03-JUN-2003; 2003US-0474940P.
 XX
 PA (INVI-) INVITROGEN CORP.
 PA (BENN/) BENNETT R P.
 PA (WELC/) WELCH P J.
 PA (HARM/) HARWOOD S.
 PA (MADD/) MADDEN K.
 PA (FRIM/) FRIMPONG K.
 PA (FRAN/) FRANKIE K E.
 XX
 PI Bennett RP, Welch PJ, Harwood S, Madden K, Frimpong K, Franke KE;
 XX
 DR WPI; 2004-132944/13.
 XX
 XX Novel nucleic acid molecule comprising all or a portion of one or more
 PT viral genome and further comprising two or more recombination sites that
 PT do not substantially recombine with each other, useful as gene therapy.
 XX
 PS Disclosure; Fig 16; 555bp; English.
 PS
 XX
 CC The invention comprises a nucleic acid molecule consisting of all or a
 CC portion of one or more viral/baculoviral genomes and further containing
 CC at least two recombination sites that do not substantially recombine with
 CC each other. One or more of the recombination sites is capable of
 CC undergoing recombination with a compatible recombination site in the
 CC presence of one or more proteins active in lambda recombination. The
 CC nucleic acid of the invention replicates in prokaryotic and eukaryotic
 CC cells. The nucleic acid of the invention is useful for constructing a
 CC recombinant virus, generating replication-defective particles,
 CC preventing/inhibiting the expression of one or more genes in an organism,
 CC and are useful as gene therapy vectors. The nucleic acid of the invention
 CC is also useful for producing and expressing fusion polypeptides. The
 CC present DNA sequence represents the OpIE2 promoter that was used in the
 CC exemplification of the invention.
 CC
 XX
 SO Sequence 560 BP, 144 A, 156 C, 116 G, 144 T, 0 U, 0 Other;

Query Match Best Local Similarity 97.2%; Score 548; DB 12; Length 560;

Matches 548; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CATGATGATTAACAATGATATGCTAATGTTGTTCAACAACAATCTGTGAACGTG 60
 DB 5 CATGATGATTAACAATGATATGCTAATGTTGTTCAACAACAATCTGTGAACGTG 64
 QY TTTTCATGTTGGCCAAAGACCTTTATCTCGGTGGCCCTCCCAACCAACTTTT 120
 DB TTTTCATGTTGGCCAAAGACCTTTATCTCGGTGGCCCTCCCAACCAACTTTT 124
 QY 121 GCACTGCAAAAAACACGCTTTTGACCGCGGCCCATACATAGTACAACTGATTTC 180
 DB 125 GCACTGCAAAAAACACGCTTTTGACCGCGGCCCATACATAGTACAACTGATTTC 184

QY 181 GTAGACTATTATTAATAATAGTCTACACCGTGTATACGCTCCAAATACACTACACAC 240
DB 185 GTAGACTATTATTAATAATAGTCTACACCGTGTATACGCTCCAAATACACTACACAC 244
QY 241 ATTGAACCTTTTTCAGTGCAGAAAAAGTACGTGTGCGACAGCATAGGCGGCGCTTATC 300
DB 245 ATTGAACCTTTTTCAGTGCAGAAAAAGTACGTGTGCGACAGCATAGGCGGCGCTTATC 304
QY 301 GGGTGGCGTCTGTACGTACGAATCACTATATGGAACCGGACGAGTGTGCTTATCGT 360
DB 305 GGGTGGCGTCTGTACGTACGAATCACTATATGGAACCGGACGAGTGTGCTTATCGT 364
QY 361 GACAGAGCGCAGTCTGCTGTGCTGTAAACCGGACCGGACGCAACTCTTATGGAACA 420
DB 365 GACAGAGCGCAGTCTGCTGTGCTGTAAACCGGACCGGACGCAACTCTTATGGAACA 424
QY 421 GAGCGCGCTTCATATACGCGCGGCTTATCTCATGCGCGTGAACCGACAGAGGCGCC 480
DB 425 GAGCGCGCTTCATATACGCGCGGCTTATCTCATGCGCGTGAACCGACAGAGGCGCC 484
QY 481 GTCCCGCTTATCGCGCTTATTAATATACAGCCCGCAACGATCTGTAAACAGATTGAACAG 540
DB 485 GTCCCGCTTATCGCGCTTATTAATATACAGCCCGCAACGATCTGTAAACAGATTGAACAG 544
QY 541 CATCTGTT 548
DB 545 CATCTGTT 552

RESULT 3

AAL61306 standard; DNA; 2773 BP.

AC AAL61306;
XX 22-SEP-2003 (first entry)
DT p2ZOp2F expression vector for insect cells.
XX
XX Multimeric protein; interleukin 5; IL5; TNFalpha; inflammatory disease;
KM tumour necrosis factor alpha; gene therapy; arthritis; gene; ds.
XX
OS Unidentified.
XX MO2003042244-A2.
PD 22-MAY-2003.
PF 15-NOV-2002; 2002MO-DK000764.
PR 16-NOV-2001; 2001DK-00001702.
PR 16-NOV-2001; 2001US-0331575P.
XX
PA (PHAR-) PHARMEXA AS.
PA (KLYS-) KLYSNER S.
PA (NIEL/) NIELSEN F. S.
PA (BRAT/) BRATT T.
PA (VOLD/) VOLDORGB B.
PA (MOUR/) MOURITSEN S.
XX
PI Klynsner S, Nielsen FS, Bratt T, Voldborg B, Mouritsen S;
XX WPI; 2003-449558/42.
XX
XX New immunogenic analogue of a polymeric protein, useful for preparing a
PT composition for treating inflammatory diseases e.g. arthritis.
XX
XX Disclosure; Page 195-196; 196pp; English.
XX
XX The invention relates to immunogenic analogues of multimeric proteins
CC such as immunogenic variants of interleukin 5 (IL5) and tumour necrosis
CC factor alpha (TNF, TNFalpha) and methods for production of immunogenic

CC analogue. The immunogenic analogue is useful for preparing a composition
CC for treating inflammatory diseases, e.g., arthritis. It is also used in
CC gene therapy. The present sequence is p2ZOp2F expression vector for
CC insect cells. This sequence is used to illustrate the method of the
CC invention
XX
SQ Sequence 2773 BP; 669 A; 750 C; 673 G; 681 T; 0 U; 0 Other;

Query Match 97.2%; Score 548; DB 9; Length 2773;
Best Local Similarity 100.0%; Pred. No. 4.4e-167;
Matches 548; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGTAGATATAACAAATGATAGTGTGCTATGCTTCAACAACTCTGTGAACGTG 60
DB 5 CAGTAGATATAACAAATGATAGTGTGCTATGCTTCAACAACTCTGTGAACGTG 64
QY 61 TTTTCATGTTTGGCAACAAACACCTTTATCTCGTGGCTCCCAACAACTTTT 120
DB 65 TTTTCATGTTTGGCAACAAACACCTTTATCTCGTGGCTCCCAACAACTTTT 124
QY 121 GCACTGCAAAAAACACGCTTTTGGACGCGGGCCCATATAGTACAACTTACGTTTC 180
DB 125 GCACTGCAAAAAACACGCTTTTGGACGCGGGCCCATATAGTACAACTTACGTTTC 184
QY 181 GTAGACTATTATTAATAATAGTCTACACCGTGTATACGCTCCAAATACACTACACAC 240
DB 185 GTAGACTATTATTAATAATAGTCTACACCGTGTATACGCTCCAAATACACTACACAC 244
QY 241 ATTGAACCTTTTTCAGTGCAGAAAAAGTACGTGTGCGACGTACAGTGGCGGCTTATC 300
DB 245 ATTGAACCTTTTTCAGTGCAGAAAAAGTACGTGTGCGACGTACAGTGGCGGCTTATC 304
QY 301 GGGTGGCGTCTGTACGTACGAATCACTATATGGAACCGGACGAGTGTGCTTATCGT 360
DB 305 GGGTGGCGTCTGTACGTACGAATCACTATATGGAACCGGACGAGTGTGCTTATCGT 364
QY 361 GACAGAGCGCAGCTTCTGTGCTGTAAACCGGACCGGACGCAACTCTTATGGAACA 420
DB 365 GACAGAGCGCAGCTTCTGTGCTGTAAACCGGACCGGACGCAACTCTTATGGAACA 424
QY 421 GAGCGCGCTTCATATACGCGCGGCTTATCTCATGCGCGTGAACCGACAGAGGCGCC 480
DB 425 GAGCGCGCTTCATATACGCGCGGCTTATCTCATGCGCGTGAACCGACAGAGGCGCC 484
QY 481 GTCCCGCTTATCGCGCTTATTAATATACAGCCCGCAACGATCTGTAAACAGATTGAACAG 540
DB 485 GTCCCGCTTATCGCGCTTATTAATATACAGCCCGCAACGATCTGTAAACAGATTGAACAG 544
QY 541 CATCTGTT 548
DB 545 CATCTGTT 552

RESULT 4

ADQ48539 standard; DNA; 5038 BP.

AC ADQ48539;
XX 09-SEP-2004 (first entry)
DT
XX
XX Viral vector-related plasmid - PIB/V5-His-DBST.
DE
XX
XX viral vector; recombinant virus;
KM replication-defective particle generation; gene expression inhibition;
KM gene therapy vector; ds; plasmid.
XX
OS Unidentified.
XX
XX MO2004009768-A2.
XX
XX 29-JAN-2004.
XX

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PF 18-JUL-2003; 2003WC-US022437.
XX
PR 18-JUL-2002; 2002US-0396335P.
PR 26-JUL-2002; 2002US-0398617P.
PR 19-NOV-2002; 2002US-0427231P.
PR 24-MAR-2003; 2003US-0456496P.
PR 03-JUN-2003; 2003US-0474940P.
XX
PA (INV-) INVITROGEN CORP.
PA (BENN/) BENNETT R P.
PA (WELC/) WELCH P J.
PA (HARM/) HARWOOD S.
PA (MADD/) MADDEN K.
PA (FRIM/) FRIMPONG K.
PA (FRAN/) FRANKE K E.
XX
PI Bennett RP, Welch PJ, Harwood S, Madden K, Frimpong K, Franke KE;
XX WPI; 2004-132944/13.
XX
PT Novel nucleic acid molecule comprising all or a portion of one or more
PT viral genome and further comprising two or more recombination sites that
PT do not substantially recombine with each other, useful as gene therapy.
XX
PS Example 18; Page 395-403; 555pp; English.
XX
CC The invention comprises a nucleic acid molecule consisting of all or a
CC portion of one or more viral/baculoviral genomes and further containing
CC at least two recombination sites that do not substantially recombine with
CC each other. One or more of the recombination sites is capable of
CC undergoing recombination with a compatible recombination site in the
CC presence of one or more proteins active in lambda recombination. The
CC nucleic acid of the invention replicates in prokaryotic and eukaryotic
CC cells. The nucleic acid of the invention is useful for constructing a
CC recombinant virus, generating replication-defective particles,
CC preventing/inhibiting the expression of one or more genes in an organism,
CC and are useful as gene therapy vectors. The nucleic acid of the invention
CC is also useful for producing and expressing fusion polypeptides. The
CC present DNA sequence represents a plasmid that was used in the
CC exemplification of the invention.
XX
SQ Sequence 5038 BP; 1342 A; 1178 C; 1198 G; 1320 T; 0 U; 0 Other;
Query Match 96.9%; Score 546.4; DB 12; Length 5038;
Best Local Similarity 99.8%; Pred. No. 1.9e-16;
Matches 547; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 CATGATGATTAACATATGATGCTAATGTTGCTTCAACAACAATTCGTGAACTGTG 60
DB 1 CATGATGATTAACATATGATGCTAATGTTGCTTCAACAACAATTCGTGAACTGTG 60
QY 61 TTTTCATGTTTGGCCAAACAGCCTTTATATCTCGGTGCGCTCCGCCACCACTTTT 120
DB 61 TTTTCATGTTTGGCCAAACAGCCTTTATATCTCGGTGCGCTCCGCCACCACTTTT 120
QY 121 GCATCGCAAAAAAAGCAGCTTTTGCACGCGGGCCCATACATATGATGAACTCTTAC 180
DB 121 GCATCGCAAAAAAAGCAGCTTTTGCACGCGGGCCCATACATATGATGAACTCTTAC 180
QY 121 GCATCGCAAAAAAAGCAGCTTTTGCACGCGGGCCCATACATATGATGAACTCTTAC 180
DB 121 GCATCGCAAAAAAAGCAGCTTTTGCACGCGGGCCCATACATATGATGAACTCTTAC 180
QY 181 GTAGACTATTTTACATTAATAGTCTACACCGTTGTATAGCTCCAAATACATACAC 240
DB 181 GTAGACTATTTTACATTAATAGTCTACACCGTTGTATAGCTCCAAATACATACAC 240
QY 241 ATTGAACCTTTTGCAGTGCAGAAAAAAGTATGTCGCGCATCAGTACGCGGCTTATC 300
DB 241 ATTGAACCTTTTGCAGTGCAGAAAAAAGTATGTCGCGCATCAGTACGCGGCTTATC 300
QY 301 GGGTCGGCTCTGTACGATGATACATTAATGAGACGAGAGTGTCTTATCGT 360
DB 301 GGGTCGGCTCTGTACGATGATACATTAATGAGACGAGAGTGTCTTATCGT 360
QY 361 GACAGAGCGCAGCTTCTGTGTGCTAACCGCAGCGGAGCGCAACTCTTATCGAACA 420
DB 361 GACAGAGCGCAGCTTCTGTGTGCTAACCGCAGCGGAGCGCAACTCTTATCGAACA 420

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DB 361 GACAGAGCGCAGCTTCTGTGTGCTAACCGCAGCGGAGCGCAACTCTTATCGAACA 420
QY 421 GAGCGGCTTCATATCAGCGCGCGCTTATCTATGCGGTACCGGACACGAGGGCCC 480
DB 421 GAGCGGCTTCATATCAGCGCGCGCTTATCTATGCGGTACCGGACACGAGGGCCC 480
QY 481 GTCCCGCTTATCGAGCTATTAATATACAGCCCGCAAGATCTGATTAACAGTTGACAG 540
DB 481 GTCCCGCTTATCGAGCTATTAATATACAGCCCGCAAGATCTGATTAACAGTTGACAG 540
QY 541 CATCTGTT 548
DB 541 CATCTGTT 548
RESULT 5
AAT13730/c
ID AAT13730 standard; DNA; 279 BP.
XX
AC AAT13730;
XX
AC 16-OCT-2003 (revised)
DT 06-SEP-1996 (first entry)
XX
DE ACNPV ORF 152, residues 132387-132109.
XX
KM Autographa californica nuclear polyhedrosis virus clone 6; disruption;
KM non-essential gene; heterologous protein production; expression vector;
KM baculovirus; ss.
XX
OS Autographa californica nucleopolyhedrovirus; clone 6.
XX
FH Key Location/Qualifiers
FT CDS 1..279
FT /tag= a
FT /note= ORF 152
FT /number= ORF 152
FT /corresponds to ACNPV nucleotides complement
FT (132387-132109)
XX
PN MO9601320-A2.
XX
PD 18-JAN-1996.
XX
PF 30-JUN-1995; 95MO-IB000578.
XX
PR 04-JUL-1994; 94GB-00013420.
XX
PA (NATU-) NATURAL ENVIRONMENT RES COUNCIL.
PI Bishop D, Possee R, Ayres M;
XX
DB WPI; 1996-087670/09.
XX
PT Autographa californica nuclear polyhedrosis virus complete genome
PT sequence - useful in the prodn. of vectors for enhanced heterologous
PT protein expression, such as interleukin(s), interferon(s) and
PT neurotoxin(s).
PS Claim 1; Page 90-186; 122pp; English.
XX
XX AAT13636-731 show open reading frames 13, 20, 22-30, 32, 38, 41-46, 50-
CC 60, 62-63, 66, 68-79, 81-87, 91-92, 96-98, 101-103, 106-127, 129-130, 140
CC - 146, 148-150, 152 and 154 from a total of 154 ORFs identified in the
CC Autographa californica nuclear polyhedrosis virus (ACNPV) clone 6. Each
CC gene is numbered according to its position in the virus genome beginning
CC at the left end of the linear map, and irrespective of its orientation.
CC The direction of transcription is relative to that of the polyhedrin
CC gene. Of the 154 ORFs identified it was found that some of the ORFs (ORFs
CC 27, 30, 32, 71, 86, 123, 126 and 127) are dispensable for virus
CC replication in cell culture or insect larvae. These genes can be deleted
CC from the genome to: (a) provide additional sites for inserting single or
CC multiple copies of foreign genes; and (b) to reduce the size of the virus
CC complementary strand relative to the polyhedrin gene. The present

```

CC sequence is designated ORF 152, and is on the complementary strand
 CC relative to the polyhedrin gene. (Updated on 16-OCT-2003 to standardise
 CC OS field)

XX Sequence 279 BP; 88 A; 36 C; 68 G; 87 T; 0 U; 0 Other;

Query Match 18.0%; Score 101.4; DB 2; Length 279;
 Best Local Similarity 75.4%; Pred. No. 2.9e-22;
 Matches 126; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

QY 112 ACTTTTTCAGTCACTGCAAAAAACAGCGCTTTTGACGCGGGCCCATATGATCAAACT 171
 DB 276 AATTTTTCGATGCAAAAAAGTTCACTTTTGCTGCACTCATATATAGTCAATCT 217

QY 172 CTACGTTTCGTAGCTATTTTACATAAATAGTCTACACCGTTGATACGCTCCAAATACA 231
 DB 216 CTCAAAATCGTAGCTATTTTATATAGATAGTCTACACGTGACATACGCTCCCAATATA 157

QY 232 CTACACACATTTGAACTTTTTCAGTGCAGTCAAAAAAGTACGTGCGC 278
 DB 156 CTACTACACTATCAACTTTTTCGATTACAAAAAGTTCAATTTTGC 110

RESULT 6
 AAT13635/c
 ID AAT13635 standard; DNA; 133894 BP.
 XX AAT13635;
 AC
 XX 16-OCT-2003 (revised)
 DT 03-SEP-1996 (first entry)
 XX
 XX ACNPV genomic DNA clone 6.
 DE
 XX Autographa californica nuclear polyhedrosis virus clone 6; disruption;
 KM non-essential gene; heterologous protein production; expression vector;
 KM baculovirus; ss.
 XX
 XX Autographa californica nucleopolyhedrovirus; clone 6.
 OS
 XX
 XX WO9601320-A2.
 PN
 XX 18-JAN-1996.
 PD
 XX 30-JUN-1995; 95MO-IB000578.
 PF
 XX 04-JUL-1994; 94GB-00013420.
 PR
 XX (NATU-) NATURAL ENVIRONMENT RES COUNCIL.
 PA
 XX Bishop D, Possee R, Ayres M;
 PI WPI; 1996-087670/09.
 DR
 XX
 XX Autographa californica nuclear polyhedrosis virus complete genome
 PT sequence - useful in the prodn. of vectors for enhanced heterologous
 PT protein expression, such as interleukin(s), interferon(s) and
 PT neurotoxin(s).
 PT
 XX
 XX Disclosure; Page 90-186; 122pp; English.
 PS
 XX
 XX The complete nucleotide sequence of the genome of clone 6 of the
 CC baculovirus Autographa californica nuclear polyhedrosis virus (ACNPV) has
 CC been determined. The sequence is taken from the Genbank record L22858.
 CC The patent specification claims a polynucleotide selected from open
 CC reading frames (ORFs 13, 20, 22-26, 28-30, 32, 38, 41-46, 50-60, 62-63,
 CC 66, 68-79, 81-87, 91-92, 96-98, 101-103, 106-126, 129-130, 140-146, 148-
 CC 150, 152 and 154 from a total of 154 ORFs identified by the patentees.
 CC See T13636-731. Expression vectors cons. the complete genomic sequence
 CC of ACNPV, with the exception that at least one non-essential ORF is
 CC disrupted or replaced are useful for the synthesis of heterologous
 CC proteins. (Updated on 16-OCT-2003 to standardise OS field)
 CC
 XX

SQ Sequence 133894 BP; 39195 A; 27151 C; 27347 G; 40201 T; 0 U; 0 Other;

Query Match 18.0%; Score 101.4; DB 2; Length 133894;
 Best Local Similarity 75.4%; Pred. No. 5.2e-21;
 Matches 126; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

QY 112 ACTTTTTCAGTCACTGCAAAAAACAGCGCTTTTGACGCGGGCCCATATGATCAAACT 171
 DB 13284 AATTTTTCGATGCAAAAAAGTTCACTTTTGCTGCACTCATATATAGTCAATCT 132325

QY 172 CTACGTTTCGTAGCTATTTTACATAAATAGTCTACACCGTTGATACGCTCCAAATACA 231
 DB 132324 CTCAAAATCGTAGCTATTTTATATAGATAGTCTACACGTGACATACGCTCCCAATATA 132265

QY 232 CTACACACATTTGAACTTTTTCAGTGCAGTCAAAAAAGTACGTGCGC 278
 DB 132264 CTACTACACTATCAACTTTTTCGATTACAAAAAGTTCAATTTTGC 132218

RESULT 7
 ADCS1646/c
 ID ADCS1646 standard; DNA; 28413 BP.
 XX ADCS1646;
 AC
 XX 18-DEC-2003 (first entry)
 DT
 XX BmNPV genomic DNA nucleotides 100001-128413.
 DE
 XX de; silkworm; silkworm movement suppression.
 KM
 XX Bombyx mori nuclear polyhedrosis virus.
 OS
 XX JP2003024062-A.
 PN
 XX 28-JAN-2003.
 PD
 XX 10-JUL-2001; 2001JP-00209305.
 PF
 XX 10-JUL-2001; 2001JP-00209305.
 PR
 XX (RIKA) RIKAKAKU KENKYUSHO.
 PA
 XX WPI; 2003-516415/49.
 DR
 XX
 XX Novel Bombyx mori polyhedrosis virus in which open reading frame gene is
 PT inactivated, or its variant, useful for suppressing movement of Bombyx
 PT mori.
 PT
 XX
 PS Claim 5; SEQ ID NO 3; 53bp; Japanese.
 PS
 XX The invention relates to a Bombyx mori (silkworm) polyhedrosis virus in
 CC which open reading frame 8 (ORF 8) gene is inactivated. The inactivated
 CC orf8 gene is useful for suppressing movement of silkworm and efficiently
 CC prevents the movement of a silkworm from a chamber in which it is raised.
 CC The present sequence is used in the exemplification of the invention.
 CC
 XX
 XX Sequence 28413 BP; 8394 A; 5713 C; 5940 G; 8366 T; 0 U; 0 Other;

Query Match 16.6%; Score 93.4; DB 10; Length 28413;
 Best Local Similarity 72.5%; Pred. No. 1e-18;
 Matches 121; Conservative 0; Mismatches 46; Indels 0; Gaps 0;

QY 112 ACTTTTTCAGTCACTGCAAAAAACAGCGCTTTTGACGCGGGCCCATATGATCAAACT 171
 DB 22231 AATTTTTCGATGCAAAAAAGTTGCGCTATGTTGACATATATATACAGTACGACT 22172

QY 172 CTACGTTTCGTAGCTATTTTACATAAATAGTCTACACCGTTGATACGCTCCAAATACA 231
 DB 22171 CTCAAAATCGTAGCTATTTTATATAGATAGTCTACACGTGACTAATACGCTTCATATA 22112

QY 232 CTACACACATTTGAACTTTTTCAGTGCAGTCAAAAAAGTACGTGCGC 278
 DB 22112

Db 22111 CTACTACTATCACTTTTGGCATTTACAAAAAGTTCATTTTGCG 22065

RESULT 8

ADQ48576
ID ADQ48576 standard; DNA; 141 BP.

XX
AC ADQ48576;

XX
DT 09-SEP-2004 (first entry)

XX
DE Viral vector-related plasmid pIB/V5-His-DEST recombination region #1.

XX
KM viral vector; recombination site; recombinant virus;

KM replication-defective particle generation; gene expression inhibition;

XX
KM gene therapy vector; ds; plasmid; recombination region.

XX
OS Unidentified.

XX
PN WO2004009768-A2.

XX
PD 29-JAN-2004.

XX
PF 18-JUL-2003; 2003WO-US022437.

XX
PR 18-JUL-2002; 2002US-0396335P.

XX
PR 26-JUL-2002; 2002US-0398617P.

XX
PR 19-NOV-2002; 2002US-0427231P.

XX
PR 24-MAR-2003; 2003US-0456496P.

XX
PR 03-JUN-2003; 2003US-0474940P.

XX
PA (INVI-) INVITROGEN CORP.

XX
PA (BENN/) BENNETT R. P.

XX
PA (WELC/) WELCH P. J.

XX
PA (HARM/) HARWOOD S.

XX
PA (MADD/) MADDEN K.

XX
PA (FRIM/) FRIMPONG K.

XX
PA (FRAN/) FRANKS K. E.

XX
PI Bennett RP, Welch PJ, Harwood S, Madden K, Frimpong K, Franke KE;

XX
DR WPI; 2004-132944/13.

XX
PT Novel nucleic acid molecule comprising all or a portion of one or more

PT viral genome and further comprising two or more recombination sites that

PT do not substantially recombine with each other, useful as gene therapy.

XX
PS Disclosure; Fig 17; 555pp; English.

XX
CC The invention comprises a nucleic acid molecule consisting of all or a

CC portion of one or more viral/baculoviral genomes and further containing

CC at least two recombination sites that do not substantially recombine with

CC each other. One or more of the recombination sites is capable of

CC undergoing recombination with a compatible recombination site in the

CC presence of one or more proteins active in lambda recombination. The

CC nucleic acid of the invention replicates in prokaryotic and eukaryotic

CC cells. The nucleic acid of the invention is useful for constructing a

CC recombinant virus, generating replication-defective particles,

CC preventing/inhibiting the expression of one or more genes in an organism,

CC and are useful as gene therapy vectors. The nucleic acid of the invention

CC is also useful for producing and expressing fusion polypeptides. The

CC present DNA sequence represents a recombination region of a plasmid that

CC was used in the exemplification of the invention.

XX
SQ Sequence 141 BP; 43 A; 36 C; 27 G; 34 T; 0 U; 1 Other;

XX
Query Match 11.0%; Score 62; DB 12; Length 141;

XX
Best Local Similarity 100.0%; Pred. No. 1.4e-09;

XX
Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX
QY 487 CTTATCGCCGCTTAAATACAGCCCGACGATCTGGTAAACACAGTTGAACAGCATCTG 546

XX
DB 1 CTTATCGCCGCTTAAATACAGCCCGACGATCTGGTAAACACAGTTGAACAGCATCTG 60

QY 547 TT 548
Db 61 TT 62

RESULT 9

ABZ10059/C
ID ABZ10059 standard; DNA; 6289 BP.

XX
AC ABZ10059;

XX
DT 16-JAN-2003 (first entry)

XX
DE Hematopoietic cell proliferation disorder related DNA sequence #199.

XX
XX Human; hematopoietic cell proliferation disorder; cytostatic;

KM gene therapy; lymphocytic leukemia; acute myelogenous leukemia;

KM cytosine methylation state; gene; ds.

XX
OS Homo sapiens.

XX
PN WO200277272-A2.

XX
PD 03-OCT-2002.

XX
PF 26-MAR-2002; 2002WO-EP003401.

XX
PR 26-MAR-2001; 2001US-0278333P.

XX
PR (EPIC-) EPIGENOMICS AG.

XX
PI Berlin K, Braun A, Disler J, Guetig D, Howe A, Mueller J;

PI Olek A, Piepenbrock C, Adorjan P, Grabs G, Iesche R, Leu B;

PI Lewin A, Lipscher E, Maier S, Model F, Mueller V, Otto T, Pelet C;

XX
PI Schwope I, Ziebarth H;

XX
DR WPI; 2003-018942/01.

XX
PT Detecting and differentiating between hematopoietic cell proliferative

PT disorders, comprises contacting a target nucleic acid with a reagent that

PT distinguishes between methylated and non-methylated CpG dinucleotides.

XX
PS Claim 28; SEQ ID NO 199; 117pp; English.

XX
CC The present invention describes a method for detecting and

CC differentiating between hematopoietic cell proliferative disorders

CC associated with at least 1 gene and/or their regulatory regions in a

CC subject. The method comprises contacting a target nucleic acid in a

CC biological sample obtained from the subject with at least 1 reagent,

CC which distinguishes between methylated and non-methylated CpG

CC dinucleotides within the target nucleic acid. ABZ0961 to ABZ1118

CC represent specifically claimed nucleotide sequences from the present

CC invention. Oligonucleotides from the present invention can be used: for

CC differentiating between healthy hematopoietic cells and proliferative

CC disorder hematopoietic cells; for differentiating between acute

CC lymphocytic leukemia and acute myelogenous leukemia; as probes for

CC determining the cytosine methylation state and/or single nucleotide

CC polymorphisms (SNPs) or hematopoietic cell proliferation disorder

CC related sequences and their complements; and as primers for the

CC application of hematopoietic cell proliferation disorder related DNA

CC sequences. The nucleotide sequences from the present invention can also

CC be used for detecting a predisposition to, differentiation between

CC subclasses, diagnosis, prognosis, treatment and/or monitoring of

CC hematopoietic cell proliferative disorders. The present method enables a

CC highly specific classification of hematopoietic cell proliferative

CC disorders allowing for improved and informed treatment of patients

XX
SQ Sequence 6289 BP; 1680 A; 178 C; 1488 G; 2943 T; 0 U; 0 Other;

XX
Query Match 7.0%; Score 39.6; DB 8; Length 6289;

XX
Best Local Similarity 53.2%; Pred. No. 0.16;

XX
Matches 84; Conservative 0; Mismatches 74; Indels 0; Gaps 0;

QY	112	AACTTTTGGCAGTCAAAAAAAGCGCTTTGGACGGGGGCCATATATGTCAACT	177		
DB	4886	AAATTATTTATTTATTAACCAATTAATACTATTAAATFCCAATACCAAAATATCATTTCAAAA	4837		
QY	172	CTACGTTTCGTAGACTATTTTACATAAATAGTCTACACCGTTGTATAGCTCAAAATACA	231		
DB	4836	TAAATATTTTAAAAACATTATTTATTAATAAATTCGTACAATTCCTTTTACTCAAAAAATA	4777		
QY	232	CTACCAACATTTGAACCTTTTGGCAGTCAAAAAAGTA	269		
DB	4776	ATACAACTTTCCTCTCCTCATTAATAAACGAAAAAATA	4739		
RESULT 10					
ID	AA546501/c				
XX	AA546501	standard; DNA; 9289 BP.			
AC	AA546501;				
DT	18-DEC-2001	(first entry)			
DE	Tumour suppressor gene derived chemically modified sequence #232.				
XX					
KW	Human; tumour suppressor gene; oncogene; antitumour; cytostatic; cancer;				
KW	tumour; CpG dinucleotide; single-nucleotide polymorphism; SNP;				
KW	cytosine methylation; ds.				
XX					
OS	Homo sapiens.				
XX					
PN	MO200168912-A2.				
PD	20-SEP-2001.				
PF	15-MAR-2001; 2001WO-EP002955.				
XX					
PR	15-MAR-2000; 2000DE-01013847.				
PR	06-APR-2000; 2000DE-01019058.				
PR	07-APR-2000; 2000DE-01019173.				
PR	30-JUN-2000; 2000DE-01032529.				
PR	01-SEP-2000; 2000DE-01043826.				
XX					
PA	(BEIG-) BEIGENOMICS AG.				
XX					
PI	Olek A, Piepenbrock C, Berlin K;				
XX					
DR	WPI; 2001-602752/68.				
PT					
PT	Fragments of chemically modified genes associated with tumor suppressor				
PT	genes and oncogenes, useful in designing primers and probes for analyzing				
XX	diseases associated with cytosine methylation state e.g. cancer.				
PS	Claim 1; SEQ ID NO 223; 27bp; English.				
XX					
CC	The invention relates to a nucleic acid comprising a sequence of 18				
CC	bases, of a segment of chemically pretreated DNA (CP DNA) e.g. with				
CC	bisulphite, of genes associated with tumour suppression and oncogenes				
CC	having a sequence taken from 536 (actually 533 since numbers 408, 458 and				
CC	500 are missing from the sequence listing) sequences (Ss) and sequences				
CC	complementary to (Ss). The nucleic acid may be a peptide nucleic acid-				
CC	oligonucleotide (PNA) of at least 9 nucleotides and may form part of a set of				
CC	probes for detecting the cytosine methylation state and/or single				
CC	nucleotide polymorphisms and also to be used in an array for analysing				
CC	diseases associated with CpG dinucleotides e.g. cancers and tumours. The				
CC	probes can also be used in a method for ascertaining genetic and/or				
CC	epigenetic parameters for the diagnosis and/or therapy of existing				
CC	diseases or the predisposition to specific diseases, by analysing				
CC	cytosine methylations. The parameters may be compared to another set of				
CC	genetic and/or epigenetic parameters, the differences serving as basis				
CC	for diagnosis and/or prognosis events which are disadvantageous to				
CC	patients. The present sequence is one of the 533 genomic sequences				
CC	derived from tumour suppressor genes and oncogenes. Note: The sequence				
CC	data for this patent did not form part of the printed specification, but				

CC	was obtained in electronic format directly from WIPO at
CC	ftp.wipo.int/pub/published_pct_sequences
XX	
SQ	Sequence 9289 BP; 2515 A; 206 C; 2097 G; 4471 T; 0 U; 0 Other;
	Query Match 7.0%; Score 39.6; DB 4; Length 9289;
	Beat Local Similarity 53.2%; Pred. No. 0.19;
	Matches 84; Conservative 0; Mismatches 74; Indels 0; Gaps 0;
QY	112 AACCTTTTGGACGCAAAAAAACACCGCTTTTGACAGCGGGGCCCATCATATGCAAACT 171
DB	7896 AATTATATTTAATATACCMAATAAAAACATTAATAATCACATCCCAATATCATTCAAAAA 7837
OY	172 CTACGTTTCGAGACGTATTTACATTAATATGTCACACCGTGTATACGTCGAATAACA 231
DB	7836 TAAATATTTTTTAAACAATTATTTATTAATAAATGTCACAAATCTTTTACTCAAAAAATA 7777
OY	232 CTACCAACATGTGAACCTTTTGGACGTCAAAAAAGTA 269
DB	7776 ATACAACTTTCCTCTCCCTATTAATAAAGCAAAAAATAA 7739
RESULT 11	
AD84121/c	
ID	AD84121 standard; DNA; 9289 BP.
XX	
AC	AD84121;
XX	
DT	29-JAN-2004 (first entry)
DE	
XX	Human lymphoid cell proliferative disorder gene derived DNA #57.
XX	
KM	ds; lymphoid cell proliferative disorder; methylation;
KM	methylated CpG dinucleotide; single nucleotide polymorphism; SNP;
KW	diffuse large B-cell lymphoma; mantle cell lymphoma;
KM	chronic lymphocytic leukemia; small lymphocytic lymphoma;
KM	follicular lymphoma; diagnosis; prognosis.
XX	
OS	Homo sapiens.
XX	
PN	WO2003044226-A2.
XX	
PD	30-MAY-2003.
XX	
PF	25-NOV-2002; 2002WO-EP013265.
XX	
PR	23-NOV-2001; 2001DE-01057491.
PR	28-DEC-2001; 2001DE-01064501.
XX	
PA	(EPIG-) EPIGENOMICS AG.
XX	
P1	Burger M, Caldwell C, Genc B, Becker E, Maier S, Nimmrich I;
XX	
DR	WPI; 2003-457621/43.
XX	
PT	Detecting and differentiating between lymphoid cell proliferative
PT	disorders comprises contacting a target nucleic acid with at least one
PT	reagent that distinguishes between methylated and non-methylated CpG
PT	dinucleotides.
XX	
PS	Claim 26; SEQ ID NO 117; 448bp; English.
XX	
CC	The invention relates to a method of detecting and differentiating
CC	between lymphoid cell proliferative disorders associated with at least
CC	one gene and/or their regulatory regions in a subject by contacting a
CC	target nucleic acid in a biological sample obtained from the subject with
CC	at least one reagent or series of reagents that distinguish between
CC	methylated and non-methylated CpG dinucleotides within the target nucleic
CC	acid. The genes and/or their regulatory regions are preferably selected
CC	from MDRI, CSNK2B, EGFR, AR, CDK4, RB2, CDC25A, GP1B beta, MYD1, CDH3,
CC	MYCL1, ELK1, ABIL1, APC, BCL2, COH1, CDKN1A, CDKN1B, CDKN2A, FOS,
CC	GSPF1, HIC-1, MGMT, MLH1, MOS, MYC, PTEN, RBL2, TGFBP2, TP73, CDKN1C,
CC	GSK3beta, ESRL1, APPL1, BAK1, BAX or HOXA5. Oligomers, peptide nucleic

CC acid (PNA)-oligomers and/or isolated nucleic acids based on the sequences
 CC of the genes are useful for detecting the methylation state of all the
 CC CpG dinucleotides within one or more the sequences, or their complements,
 CC for determining the cytosine methylation state and/or single nucleotide
 CC polymorphisms (SNPs), and for differentiating at least two of the medical
 CC conditions such as diffuse large B-cell lymphoma, mantle cell lymphoma,
 CC chronic lymphocytic leukemia, small lymphocytic lymphoma and follicular
 CC lymphoma. They are also useful for detecting of a predisposition to,
 CC differentiation between subclasses, diagnosis, prognosis, treating and/or
 CC monitoring of lymphoid cell proliferative disorder. This sequence
 CC represents a nucleic acid of a pretreated genomic DNA derived from the
 CC above mentioned genes.

SQ Sequence 9289 BP; 2515 A; 206 C; 2097 G; 4471 T; 0 U; 0 Other;

Query Match 7.0%; Score 39.6; DB 10; Length 9289;
 Best Local Similarity 53.2%; Pred. No. 0.19;
 Matches 84; Conservative 0; Mismatches 74; Indels 0; Gaps 0;

Dy 112 AACTTTTTCGACGTCGCAAAAAACAGCGCTTTGACAGCGGGCCCATCATGTGCAAACT 171
 Db 7896 AATTATTTTATATACCAAAATTAACATATTAATCCACTACCAAAATATCATTCAGAAAA 7837

Dy 172 CTACGTTTCGTAGACTATTTTACATTAATAGTCTACACCGTGTATACGCTCAAAATACA 231
 Db 7836 TAATTAATTTTAAACATTTATTTTAAATAATCGTCACAAATCTTTTACTCAAAAAATA 7777

Dy 232 CTACACACATTTGAACCTTTTTCGACGTGCAAAAAAGTA 269
 Db 7776 ATACAACTTTCCTCCTCCCTATTAACGAAAAATAAATA 7739

RESULT 12
 ABZ10205/c
 ID ABZ10205 standard; DNA; 6289 BP.

XX ABZ10205;

DT 16-JAN-2003 (first entry)

DE Haematopoietic cell proliferation disorder related DNA sequence #345.

XX Human; haematopoietic cell proliferation disorder; cytostatic;
 KM Gene therapy; lymphocytic leukemia; acute myelogenous leukaemia;
 KM cytosine methylation state; gene; ds.

OS Homo sapiens.

PN WO20027272-A2.

PD 03-OCT-2002.

PF 26-MAR-2002; 2002WO-EP003401.

PR 26-MAR-2001; 2001US-0278333P.

XX (EPIG-) EPIGENOMICS AG.

PI Berlin K, Braun A, Distler J, Guetig D, Howe A, Mueller J;
 PI Olek A, Pleschbrock C, Adorjan P, Grabs G, Liesche R, Leu B;
 PI Lewin A, Lipscher B, Maier S, Model F, Mueller V, Otto T, Pelet C;
 PI Schwabe I, Ziebarth H;

DR WPI; 2003-018942/01.

XX Detecting and differentiating between hematopoietic cell proliferative
 PT disorders, comprises contacting a target nucleic acid with a reagent that
 PT distinguishes between methylated and non-methylated CpG dinucleotides.

XX Claim 28; SEQ ID NO 345; 117bp; English.

XX The present invention describes a method for detecting and
 CC differentiating between haematopoietic cell proliferative disorders

CC associated with at least 1 gene and/or their regulatory regions in a
 CC subject. The method comprises contacting a target nucleic acid in a
 CC biological sample obtained from the subject with at least 1 reagent,
 CC which distinguishes between methylated and non-methylated CpG
 CC dinucleotides within the target nucleic acid. ABZ09861 to ABZ1118
 CC represent specifically claimed nucleotide sequences from the present
 CC invention. Oligonucleotides from the present invention can be used: for
 CC differentiation between healthy haematopoietic cells and proliferative
 CC disorder haematopoietic cells; for differentiating between acute
 CC lymphocytic leukaemia and acute myelogenous leukaemia; as probes for
 CC determining the cytosine methylation state and/or single nucleotide
 CC polymorphisms (SNPs) of haematopoietic cell proliferation disorder
 CC related sequences and their complements; and as primers for the
 CC amplification of haematopoietic cell proliferation disorder related DNA
 CC sequences. The nucleotide sequences from the present invention can also
 CC be used for detecting a predisposition to, differentiation between
 CC subclasses, diagnosis, prognosis, treatment and/or monitoring of
 CC haematopoietic cell proliferative disorders. The present method enables a
 CC highly specific classification of haematopoietic cell proliferative
 CC disorders allowing for improved and informed treatment of patients

SQ Sequence 6289 BP; 1680 A; 0 C; 1488 G; 3121 T; 0 U; 0 Other;

Query Match 6.7%; Score 38; DB 8; Length 6289;
 Best Local Similarity 52.5%; Pred. No. 0.53;
 Matches 83; Conservative 0; Mismatches 75; Indels 0; Gaps 0;

Dy 112 AACTTTTTCGACGTCGCAAAAAACAGCGCTTTGACAGCGGGCCCATCATGTGCAAACT 171
 Db 4896 AATTATTTTATATACCAAAATTAACATATTAATCCACTACCAAAATATCATTCAGAAAA 4837

Dy 172 CTACGTTTCGTAGACTATTTTACATTAATAGTCTACACCGTGTATACGCTCAAAATACA 231
 Db 4836 TAATTAATTTTAAACATTTATTTTAAATAATCATCAATTTTCTTACTCAAAAAATA 4777

Dy 232 CTACACACATTTGAACCTTTTTCGACGTGCAAAAAAGTA 269
 Db 4776 ATACAACTTTCCTCCTCCCTATTAACGAAAAATAAATA 4739

RESULT 13
 ADEB84197/c
 ID ADEB84197 standard; DNA; 9289 BP.

XX ADEB84197;

DT 29-JAN-2004 (first entry)

DE Human lymphoid cell proliferative disorder gene derived DNA #133.

XX de; lymphoid cell proliferative disorder; methylation;
 KM methylated CpG dinucleotide; single nucleotide polymorphism; SNP;
 KM diffuse large B-cell lymphoma; mantle cell lymphoma;
 KM chronic lymphocytic leukemia; small lymphocytic lymphoma;
 KM follicular lymphoma; diagnosis; prognosis.

OS Homo sapiens.

PN WO2003044226-A2.

PD 30-MAY-2003.

PF 25-NOV-2002; 2002WO-EP013265.

PR 23-NOV-2001; 2001DE-01057491.

PR 28-DEC-2001; 2001DE-01064501.

XX (EPIG-) EPIGENOMICS AG.

PI Burger M, Caldwell C, Genc B, Becker E, Maier S, Nimmrich I;

DR WPI; 2003-457621/43.

PT Detecting and differentiating between lymphoid cell proliferative
 PT disorders comprises contacting a target nucleic acid with at least one
 PT reagent that distinguishes between methylated and non-methylated CpG
 PT dinucleotides.
 PS Claim 26; SEQ ID NO 193; 448bp; English.
 XX
 CC The invention relates to a method of detecting and differentiating
 CC between lymphoid cell proliferative disorders associated with at least
 CC one gene and/or their regulatory regions in a subject by contacting a
 CC target nucleic acid in a biological sample obtained from the subject with
 CC at least one reagent or series of reagents that distinguish between
 CC methylated and non-methylated CpG dinucleotides within the target nucleic
 CC acid. The genes and/or their regulatory regions are preferably selected
 CC from MDR1, CSNK2B, EGR4, AR, CDK4, RB2, CDC25A, GP1b beta, MYO1, CD13,
 CC MYCL1, ELK1, ABL1, APC, BCL2, CDH1, CDKN1A, CDKN1B, CDKN2A, CDKN2B, FOS,
 CC GSTR1, HIC-1, MGMT, MTH1, MOS, MYC, PTEN, RBL2, TGFB2, TP73, CDKN1C,
 CC GSK3beta, ESRI, APAF1, BAK1, BAX or HOXA5. Oligomers, peptide nucleic
 CC acid (PNA)-oligomers and/or isolated nucleic acids based on the sequences
 CC of the genes are useful for detecting the methylation state of all the
 CC CpG dinucleotides within one or more the sequences, or their complements,
 CC for determining the cytosine methylation state and/or single nucleotide
 CC polymorphisms (SNPs), and for differentiating at least two of the medical
 CC conditions such as diffuse large B-cell lymphoma, mantle cell lymphoma,
 CC chronic lymphocytic leukemia, small lymphocytic lymphoma and follicular
 CC lymphoma. They are also useful for detecting of a predisposition to,
 CC differentiation between subclasses, diagnosis, prognosis, treating and/or
 CC monitoring of lymphoid cell proliferative disorder. This sequence
 CC represents a nucleic acid of a pretreated genomic DNA derived from the
 CC above mentioned genes.
 XX
 SQ Sequence 9289 BP; 2515 A; 0 C; 2097 G; 4677 T; 0 U; 0 Other;
 Query Match 6.7%; Score 38; DB 10; Length 9289;
 Best Local Similarity 52.5%; Pred. No. 0.63; Indels 0; Gaps 0;
 Matches 83; Conservative 0; Mismatches 75; Indels 0; Gaps 0;
 QY 112 AACTTTTTCACGCAAAAACAGCGTTTGCAGCGGGCCCATACATGATCAACT 171
 Db 7896 AATTATTTTATTAACCAATTAACATATTAATCACTACCAATATCATTCAAAA 7837
 QY 172 CTACGTTTCGTAGACATTTTACATAATAGTCTACACGCTGTATACGCTCAAAATACA 231
 Db 7836 TAATATTTTAAAAACATTTATTAATAAATCATCAATCTCTTTTACTCAAAAAATA 7777
 QY 232 CTACCAACATTAACCTTTTTCAGTGCAGAAAAAGTA 269
 Db 7776 ATACAACCTTCTCTCCCTATAAAAAACAAAAAATA 7739
 RESULT 14
 ACL35887
 ID ACL35887 standard; cDNA; 2000 BP.
 XX
 AC ACL35887;
 XX
 DT 02-JUN-2005 (first entry)
 XX
 DE Rice stress-regulated promoter SEQ ID NO:14450.
 XX
 KW as; abiotic stress tolerance; transgenic plant; plant; cereal;
 XX agriculture.
 XX
 OS Oryza sativa.
 XX
 PN WO2003008540-A2.
 XX
 PD 30-JAN-2003.
 XX
 PF 21-JUN-2002; 2002WO-US019668.
 XX
 PR 22-JUN-2001; 2001US-0300112P.
 XX
 PR 24-AUG-2001; 2001US-0314662P.

PR 26-SEP-2001; 2001US-0325277P.
 PR 21-NOV-2001; 2001US-0332132P.
 XX
 XX (SYGN) SYNGENTA PARTICIPATIONS AG.
 PA
 XX Keps J, Briggs SP, Cooper B, Glazebrook J, Goff SA, Katagiri F,
 PI Moughamer T, Provart N, Riecke D, Zhu T;
 XX WPI; 2003-248011/24.
 DR
 XX
 XX New stress-responsive nucleic acid, useful for altering the
 PT responsiveness of a plant, e.g. cereal, to an abiotic stress such as cold
 PT stress, salt stress or osmotic stress.
 XX
 PS Claim 48; SEQ ID NO 14450; 89bp; English.
 XX
 CC The invention relates to novel abiotic stress responsive polynucleotides
 CC and polypeptides. Also disclosed are vectors, expression cassettes, host
 CC cells, and plants containing such polynucleotides. Also disclosed are
 CC methods for using the polynucleotides and polypeptides to alter the
 CC responsiveness of a plant to abiotic stress. The invention is useful in
 CC agriculture. The nucleic acid is useful for determining whether a test
 CC plant has been exposed to an abiotic stress condition. It is also useful
 CC for selecting an agent that alters abiotic stress regulated
 CC polynucleotide expression in a plant cell, and to identify a homolog or
 CC ortholog to an abiotic stress responsive polynucleotide. The nucleic acid
 CC molecule and the polypeptide encoded by it are useful in altering the
 CC responsiveness of a plant to an abiotic stress, such as cold stress, salt
 CC stress, osmotic stress or any of their combinations. The present sequence
 CC is used in the exemplification of the invention
 XX
 SQ Sequence 2000 BP; 410 A; 329 C; 253 G; 416 T; 0 U; 592 Other;
 Query Match 6.6%; Score 37.4; DB 11; Length 2000;
 Best Local Similarity 16.0%; Pred. No. 0.49;
 Matches 69; Conservative 155; Mismatches 207; Indels 0; Gaps 0;
 QY 5 ATGATAAACAAGTATAGTGCTAATGCTTGCCTTCAACAAATTCGTGAAGTGTGTTT 64
 Db 104 WKRYKMMWAKWATKMYKMYVATTTTTRTCACCMKMMWAGMYGTGVRATTKMYMAT 163
 QY 65 CANGTTTGCAACAACACACTTATATCGGTGGGCTCCCAACACAACTTTTGGCAC 124
 Db 164 CACTCTKTKWKKWRMRMSAWTGSWRTCAAMBAWMTYSWMBRCAAAGTGTGCRNA 223
 QY 125 TGCAAAAAACAAGCTTTTGCACGCGGCCCATATACATAGTAACTTACGTTTGTAG 184
 Db 224 GRWCATMTTWTGRTTCAGMMWKMSYMGKCAVATMYMRKRMYTAAAMTACTYRT 283
 QY 185 ACTATTTTACATATAATAGTCTACACCGTGTATACGCTCAATAATACATACACACATTG 244
 Db 284 GMYWCMKRAAAMWASAYTTAMMMWTKTAYWMCAGRAACAAVMMWMMWMMWMMWMMW 343
 QY 245 AACCTTTTGCAGTGAATAAAGTACGTGCGGACGTACGTAAGCGGCGCTTATGGGT 304
 Db 344 SAAVARMAMMTTATCTAAMMYTMSCRYKMKZAMMAAAYMTMRRTMACTTAAXKRMAC 403
 QY 305 CGGCTCTGTCAGTGAATCAATATTCGACCGACGAGAGTGTGCTTATCGTGACA 364
 Db 404 YGACMAAMCAVAGMTTCBSTYARTMAAGRCRASGCMAAMCTMTYKRYMTETRAAGMNA 463
 QY 365 GGAAGCCAGCTTCGTGTGTGTTAACCAGGACGCGGACGCACTCTCTTATCGAAGCAGAC 424
 Db 464 WKKCYMMWMSMATWTKYMYTMYRMASKMATTKCYCSACAYWYRCWKYRKYRAMGMAY 523
 QY 425 GCGCCTCCATA 435
 Db 524 WGCYSMTCAVA 534
 RESULT 15
 ADA71938/C
 ID ADA71938 standard; DNA; 2000 BP.

XX ADA71938;
XC
AC 20-NOV-2003 (first entry)
XT
DT Rice gene, SEQ ID 5263.
DE Plant; bacterial infection; fungal infection; viral infection; rice,
KM gene; ds.
OS Oryza sativa.
XN WO2003000898-A1.
PX
PO 03-JAN-2003.
PF 22-JUN-2001; 2001WO-IB001105.
PP 22-JUN-2001; 2001WO-IB001105.
PR 22-JUN-2001; 2001WO-IB001105.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
PI Chang H, Chen W, Cooper B, Glaesbrook J, Goff SA, Hou Y,
FI Kacagiti F, Qian S, Tao Y, Whitcomb S, Xie Z, Zhu T, Zou G;
XX WP1; 2003-175290/17.
DR
XX Identifying at least one gene involved in plant resistance or response to
PT pathogenic infection for conferring resistance or tolerance to a plant to
PT bacterial, fungal or viral infection by determining or detecting plant
FT gene expression.
PS
XS Claim 27; SEQ ID NO 5263; 899pp; English.
CC
XX The present invention relates to a method (M1) for identifying genes
CC involved in plant resistance or response to pathogenic infection. M1
CC comprises identifying a gene whose expression is significantly altered in
CC the incompatible interaction of plant gene expression relative to
CC the expression of the gene in an uninfected plant, in a mutant plant that
CC does not express a gene associated with response to pathogenic infection,
CC or in a corresponding incompatible or compatible interaction. (M1) is
CC useful for conferring resistance to resistance or tolerance to a plant to
CC bacterial, fungal or viral infection. The present sequence was used to
CC illustrate the invention.
CX
CO Sequence 2000 BP; 336 A; 265 C; 284 G; 363 T; 0 U; 752 Other;

Query Match 6.4%; Score 36.2; DB 8; Length 2000;
Best Local Similarity 11.3%; Pred. No. 1.2;
Matches 42; Conservative 169; Mismatches 157; Indels 3; Gaps 1

DY 124 CTGCAAAAAAACAGCGCTTTTGCACGGCGGCCCATATCATGTACAATAACTTCATCGTTTGTA 183
|||:::||||:||||:||||:||||:||||:||||:||||:
Db 430 CYGCGMTMYCYGYMKWTYMGSYKRSCKYKRMYMMYGWVMYYSAVSMMTMYYXY 371
:::||||:||||:||||:||||:||||:||||:||||:
Dy 184 GACATTATTACATAAATAGTACACCGETTGATAGOGCTCCAATAATACACTACACAAATT 243
:::||||:||||:||||:||||:||||:||||:||||:
370 AKYMKTYKKRKGTHSMVGSKKYKC---TWCMYKMCRTWRKOMRKTKYSKRCICW 314
:::||||:||||:||||:||||:||||:||||:||||:
Dy 244 GAACCTTTTTGCAGTGAACAAAAGAATAGCGTGTGCGAGTCACTAGCGCGCCTTATCGGG 303
|||:::||||:||||:||||:||||:||||:||||:||||:
Db 313 RYATCYWCVCYRKRGWYRSBRSMRTAKWKMSWSMRCSYSWMYVKMWKKSYYMSG 254
:::||||:||||:||||:||||:||||:||||:||||:
Dy 304 TCgcctcctgcaactgaatcatattatggaccgccagcgagtgttgttttatgtctaac 363
:::||||:||||:||||:||||:||||:||||:||||:
253 WARSSGTVSRSAAKRYTGYSTSRRAKMMRAMCRMSACKRRYSRTYSYGCSYCGSSKMXY 194
:::||||:||||:||||:||||:||||:||||:||||:
Dy 364 AGAAGCCAGAGCTTCTGTGTGTTCTAAACGGCACGGACGCAACTCTTATCGGAACAGGA 423
|||:::||||:||||:||||:||||:||||:||||:||||:
Db 193 MSKSSMMNTGSSWNSCCCTCYGGAMCMSCCMSMMYMGSCGYTGWKMKRSYKSMCKKY 134
|||:::||||:||||:||||:||||:||||:||||:||||:
424 CGCGCTTCATATCAGCGCGCGGCTTATCTCATGCGGTGACGGACAGAGCGCCCCTC 483
|||:::||||:||||:||||:||||:||||:||||:||||:

Db	QY	Db
133	484	73
CSGCTKACSTGTYRRICKMTKISYYKCYICVCTWTSYMRKMKCMCSGSSNMSCAYC	CCGCTTATCGC	STSTSTSMMSM
	494	63
	::: :::	
	73	
	STSTSTSMMSM	
	63	

Search completed: June 15, 2006, 16:31:49
Job time : 608.079 secs

GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: June 15, 2006, 16:32:06 ; Search time 4719.79 Seconds
(without alignments)
6682.184 Million cell updates/sec

Title: US-09-896-888a-1
Perfect score: 564
Sequence: 1 catgatgatacaacatcatat.....tggtacagcgacacacatg 564

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 48236798 seqs, 27959665780 residues
Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
EST:*
1: gb_est1:*
2: gb_est3:*
3: gb_est4:*
4: gb_est5:*
5: gb_est6:*
6: gb_est7:*
7: gb_est8:*
8: gb_est9:*
9: gb_est10:*
10: gb_est11:*
11: gb_est12:*
12: gb_est13:*
13: gb_est14:*
14: gb_est15:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	81.2	14.4	679	1	AV398660
2	41.4	7.3	883	13	DUA36534
3	39.6	7.0	984	12	CL0772394
4	39	6.9	762	14	BX147578
5	39	6.9	1324	12	CG751412
6	38.6	6.8	758	11	BH517933
7	38.2	6.8	535	10	N63392
8	38	6.7	578	12	BZ902838
9	38	6.7	582	12	BZ899636
10	37.6	6.7	583	14	DX064229
11	37.2	6.6	425	4	CB410241
12	37.2	6.6	669	8	CO384338
13	37	6.5	822	9	DN873866
14	36.8	6.5	576	8	CV918268
15	36.8	6.5	1101	14	CNS0039X
16	36.6	6.5	432	1	AI437474
17	36.6	6.5	580	2	BI843287
18	36.6	6.5	1032	6	CNS0GAMP
19	36.4	6.5	480	4	CB484581

20	36.4	6.5	857	12	CG935894	CG935894 MBEAV05TR
21	35.8	6.3	461	11	BH757407	BH757407 SALX_0561
22	35.8	6.3	655	14	AG358704	AG358704 Mus Tribu
23	35.8	6.3	675	2	BG695019	BG695019 NISC_1v11
24	35.8	6.3	715	7	BE374425	BE374425 601227596
25	35.8	6.3	1049	13	CL510716	CL510716 SAHL_836
26	35.6	6.3	516	2	BM278655	BM278655 Ag tgz 65
27	35.6	6.3	613	13	CL753134	CL753134 OE_BBA012
28	35.6	6.3	626	14	AG401197	AG401197 Mus muscu
29	35.6	6.3	665	13	CL742215	CL742215 OR_BBA007
30	35.6	6.3	761	13	CM655793	CM655793 OG_BBA000
31	35.6	6.3	764	9	DN808697	DN808697 76814387
32	35.6	6.3	787	11	A0857977	A0857977 nbe0011D
33	35.6	6.3	803	9	CX336435	CX336435 JGI_X2T19
34	35.6	6.3	1080	14	CNS02APV	AL188860 Tetradon
35	35.4	6.3	755	11	AQ751255	AQ751255 HS_5574_B
36	35.4	6.3	835	5	CK706618	CK706618 ZF101_P00
37	35.4	6.3	997	12	CG020891	CG020891 ZMMBB055
38	35.2	6.2	579	2	CV968528	CV968528 PC063R8_1
39	35.2	6.2	815	12	CG861440	CG861440 NDL_122K2
40	35.2	6.2	1019	2	BG247625	BG247625 602359311
41	35.2	6.2	1101	14	CNS00LO0	AL068607 Drosophila
42	35	6.2	589	2	BM525801	BM525801 sak72a09
43	35	6.2	780	14	AG394612	AG394612 Mus muscu
44	35	6.2	972	9	DN909117	DN909117 57860_3 D
45	35	6.2	988	14	CNS0067B	AL062985 Drosophila

ALIGNMENTS

RESULT 1
AV398660
LOCUS
DEFINITION
AV398660 Bombyx mori ovary BmNPV infected; 6 hr after inoculation
Bombyx mori cDNA clone NV060140 T3, mRNA sequence.
AV398660
ACCESSION
AV398660.1 GI:6902312
VERSION
KEYWORDS
SOURCE
ORGANISM
Bombyx mori (domestic silkworm)
Bombyx mori
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Lepidoptera; Glossata; Dictyoptera;
Bombycoidea; Bombycidae; Bombyx.
1 (bases 1 to 679)
Mita,K., Morimoto,M., Shimada,T., Okano,K. and Maeda,S.
Bombyx mori cDNA
Unpublished (2000)
Contact: Mita K
Genome Research Group
National Institute of Agrobiological Sciences
Owashi 1-2, Tsukuba, Ibaraki 305-8634, Japan
Tel: 81-29-838-6120
Fax: 81-29-838-6121
Email: kmits@ias.affrc.go.jp
Project: "Silkworm Genome Program in MAF, and Research for the
Future Program in JSPS". see "Silkbase",
http://www.ab.a.u-tokyo.ac.jp/silkbase/, for whole ESTdb.
Location/Qualifiers
1..679
/organism="Bombyx mori"
/mol_type="mRNA"
/db_xref="taxon:7091"
/clone="NV060140"
/issue_type="ovary"
/cell_type="BmNPV infected; 6 hr after inoculation"
/dev_stage="BmNPV infected; 6 hr after inoculation"
/clone_11b="Bombyx mori ovary BmNPV infected; 6 hr after inoculation"

ORIGIN
Query Match 14.4%; Score 81.2; DB 1; Length 679;
Best Local Similarity 71.3%; Pred. No. 3.1e-14;

Matches 107; Conservative 0; Mismatches 43; Indels 0; Gaps 0;

QY 129 AAAAAACAGCTTTGACAGCGGCGCCATACATAGTACAACTTACTTTCGAGCTA 188
 DB 1 AAAAAAGTCCGCTATGTTTACATATATATACAGTACGAACTCTACAAAATCGAGACTA 60

QY 189 TTTTACATAATAGTCTACACCGCTGTATAGCTCCAAATACACTACACACATTGGAAC 248
 DB 61 TTTTATAGAAATAGTCTACACTGTACATAGCTCTCAATATACTACTACATCACTCACT 120

QY 249 TTTTTCAGTGCACAAAAGTACGTGTGCGC 278
 DB 121 TTTTTCAGTGCACAAAAGTACATTTTTCG 150

RESULT 2
 DU436534/c 883 bp DNA linear GSS 06-OCT-2005
 LOCUS 1098415929593 CHORI-243 Ovis aries genomic clone CH243-284G6,
 DEFINITION genomic survey sequence.
 ACCESSION DU436534 GI:77190412
 VERSION DU436534.1
 KEYWORDS GSS.
 SOURCE Ovis aries (sheep)
 ORGANISM Ovis aries
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
 Pecora; Bovidae; Caprinae; Ovis.
 1 (bases 1 to 883)
 Kikines,E., Shetty,J., de Jong,P., McEwan,J.C., Oddy,H. and
 Cockett,N.
 Ovine BAC End Sequences from Library CHORI-243
 Unpublished (2004)
 Other_GSSs: 1098421042324
 Contact: Ewen Kikines
 The Institute for Genomic Research (TIGR; www.tigr.org)
 9712 Medical Center Drive, Rockville, MD 20850, USA
 Tel: 301-795-7536
 Email: ekikines@tigr.org
 Sequences generated at the J. Craig Venter Institute Joint
 Technology Center (JCVI/JTC; http://www.venterlinstitute.org/).
 Original trace: 1098415929593 Trace TI: gnl|tl|918980430
 Insert Length: 184000 Std Error: 0.00 row: G column: 6
 Seq Primer: T7
 Class: BAC ends

FEATURES
 Location/Qualifiers
 1..883
 /organism="Ovis aries"
 /mol_type="genomic DNA"
 /strain="Texel breed"
 /db_xref="taxon:9940"
 /clone="CH243-284G6"
 /sex="Male"
 /cell_type="Blood"
 /clone_lib="CHORI-243"
 /notes="Vector: PTARBAC2.1; Site 1: EcoRI; Site 2: EcoRI;
 The CHORI-243 sheep (M) (Ovis aries) BAC library produced
 by Pieter de Jong's lab at CHORI
 http://bacpac.chori.org/library.php?id=162"

ORIGIN
 Query Match 7.3%; Score 41.4; DB 13; Length 883;
 Best Local Similarity 55.1%; Pred. No. 0.18; Mismatches 66; Indels 0; Gaps 0;
 Matches 81; Conservative 0; Mismatches 66; Indels 0; Gaps 0;

QY 1 CATGATGATTAACAGATGATGCTAATGTTGCTTCAACAACAATTCGTGTAACCTG 60
 DB 162 CATGCTGATCAATGAGGCAATAAATGTTGTTATAGACACATTTGTGAATGTA 103

QY 61 TTTTCATGTTGGCAACAAGCACTTATATCTGCTGCGCTCCGCCACCAACATTTT 120
 DB 102 TTACCAAGCTTTTAAACACCACTTTATGTTTGGACCTTAATCATCACCAATGAAT 43

QY 121 GCACTGCAAAAAAAGCGCTTTTGAC 147
 DB 42 TCACATTAATAAAAAAGGAGTTTCTC 16

RESULT 3
 CL077394 954 bp DNA linear GSS 31-DEC-2003
 LOCUS CH216-145B11_Sp6.1 CH216 Xenopus tropicalis genomic clone
 DEFINITION CH216-145B11, genomic survey sequence.
 ACCESSION CL077394.1 GI:40533307
 VERSION CL077394.1
 KEYWORDS GSS.
 SOURCE Xenopus tropicalis (western clawed frog)
 ORGANISM Xenopus tropicalis
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
 Xenopodinae; Xenopus; Silurana.
 1 (bases 1 to 954)
 Kremitzki,C., Carter,J., McPherson,J., Warren,W., Graves,T.,
 Mardis,E. and Wilson,R.
 A physical map of the xenopus tropicalis genome
 Unpublished (2003)
 Contact: Richard K Wilson
 Genome Sequencing Center
 Washington University School of Medicine
 Email: submissions@wustl.wustl.edu
 Insert Length: 175000 Std Error: 0.00
 Seq primer: Sp6 ATTTAGTGACACTATAG
 Class: BAC ends
 High quality sequence start: 163
 High quality sequence stop: 226.

FEATURES
 Location/Qualifiers
 1..954
 /organism="Xenopus tropicalis"
 /mol_type="genomic DNA"
 /strain="Nigerian frog"
 /db_xref="taxon:8364"
 /clone="CH216-145B11"
 /sex="male"
 /cell_line="Stock 248 F7A2, inbred N7"
 /clone_lib="CH216"
 /notes="Vector: PTARBAC2.1; CHORI-216 Xenopus tropicalis
 BAC library"

ORIGIN
 Query Match 7.0%; Score 39.6; DB 12; Length 954;
 Best Local Similarity 52.4%; Pred. No. 0.71; Mismatches 79; Indels 0; Gaps 0;
 Matches 87; Conservative 0; Mismatches 79; Indels 0; Gaps 0;

QY 103 CCACACACCAACTTTTGGACACTGCACAAAACAGCGCTTTGCGCGGCGCCATACATA 162
 DB 330 CGCCCCCCCCCTTTTGTATACAAAABACACCCCTCTTCAACCCACCTTAACATA 389

QY 163 GTACAACTCTAGCTTTCGTAGACTATTTTACATAATAGTCTACACCGTTGTATAGCT 222
 DB 390 ATGTGAAGCTCTATTTATCACTATATATTAACGATATGATGCCCTGACGTAAATC 449

QY 223 CCAATATACACTACACACATTTGAACTTTTGGACGTGCAAAAAGT 268
 DB 450 ATTAAGATATATACACTGACTGACTCTCTGTATCCATATTAAT 495

RESULT 4
 BX147578/c 762 bp DNA linear GSS 28-JAN-2003
 LOCUS BX147578
 DEFINITION Danio rerio genomic clone DKEX-10914, genomic survey sequence.
 ACCESSION BX147578
 VERSION BX147578.1 GI:27978953
 KEYWORDS GSS.
 SOURCE Danio rerio (zebrafish)
 ORGANISM Danio rerio
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

```

/notes="The library was generated by a partial digest of
the genomic DNA with EcoRI and cloning into the BAC
vector."
ORIGIN
Query Match          6.9%; Score 39; DB 12; Length 1324;
Best Local Similarity 48.1%; Pred. No. 1.2;
Matches 111; Conservative 0; Mismatches 120; Indels 0; Gaps 0;
Qy 38 AACACAATTCGTTGGAAGTGTGTTTCATGTTTGCCACAGACCTTTATCTCGGTG 97
Db 1092 AATATGACCAACCTTTTAATCTTTTTTTTTTTTTTTTCTGGAACCCCTTTTAACCTCC 1151
Qy 98 GCCTCCCAACCAACCACTTTTTCACCTGCAAAAAACAGCTTTTGACGCGGCCCAT 157
Db 1152 TCCTTAGTAAACCCCAAAAGTTGGAATTCATATACGAGGCCCTTTAAATTAATCA 1211
Qy 158 ACATAGTACAAACCTCTACGTTTGTGTAGTACTATTTTACATAATAGTCTACACGTTGAT 217
Db 1212 AGAATATCCCACTAGCTTAAAGGAAATTAATTCAAAAAAAATATTCCTTTATTT 1271
Qy 218 ACCTCCCAATATACACTACACACACTTGAACCTTTTTCAGTCAGCAAAAAAGT 268
Db 1272 TGGAAAAAATCATTTTTCACCCCCCATATTTTTCGCCCAAAAAAGT 1322

RESULT 6
LOCUS BH517933/c 758 bp DNA linear GSS 13-DEC-2001
DEFINITION BOGBL87TF BOGB Brassica oleracea genomic clone BOGBL87, genomic
survey sequence.
ACCESSION BH517933
VERSION BH517933
KEYWORDS BH517933.1 GI:17726023
SOURCE GSS.
ORGANISM Brassica oleracea
Brassica oleracea
Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
1 (bases 1 to 758)
Aylee,M., Haas,B.J., Kumar,N., Wu,H., Xiao,Y., Van Aken,S.,
Utterback,T.R., Wortman,J.R., White,O.R. and Town,C.D.
Whole genome shotgun sequencing of Brassica oleracea and its
application to gene discovery and annotation in Arabidopsis
Genome Res. 15 (4), 487-495 (2005)
15805490
COMMENT Contact: Chris Town
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA.
Tel: 301-838-3523
Fax: 301-838-0208
Email: cdtown@tigr.org
DNA is from a doubled haploid provided by Tom Osborn.
Seq primer: TF
Class: sheared ends.
FEATURES
Location/Qualifiers
source 1..758
/organism="Brassica oleracea"
/mol_type="genomic DNA"
/strain="TO100DH3"
/db_xref="taxon:3712"
/clone="BOGBL87"
/clone_1lb="BOGB"
/notes="Vector: pHOS1, Site_1: BstXI; 2-3 kb sheared
genomic DNA inserted into pHOS1 using BstXI linkers"
ORIGIN
Query Match          6.8%; Score 38.6; DB 11; Length 758;
Best Local Similarity 52.1%; Pred. No. 1.4;
Matches 86; Conservative 0; Mismatches 79; Indels 0; Gaps 0;
Qy 110 CCAACTTTTGGACGCTGCAAAAAACACGCTTTTGACGCGGCCCATATAGTACAA 169

```

Qy	Dy	Qy	Dy
1 70	527	230	407
CTCAGCGTTTCGTA	CCAGTGGTTCAC	CACACACACAT	AAATTCATACAA
CTATTTTTCAT	CTTACAAAGAT	TCGACCTTTTG	TAATATATATGA
TAATATAGT	CTCAGTCTC	AGTCAAAAAG	ATATATATGAC
CTACCGGTTATAG	CTCATCAACAA	AGTACTGT	ATATATATGAC
CTCCAAATTA	AAATATATATAA		
467			
CTCAGCGTTTCGTA			
CTATTTTTCAT			
TAATATAGT			
CTACCGGTTATAG			
CTCCAAATTA			
407			
CTCAGCGTTTCGTA			
CTATTTTTCAT			
TAATATAGT			
CTACCGGTTATAG			
CTCCAAATTA			

RESULT 7

LOCUS N63392 535 bp mRNA linear EST 01-MAR-1996
DEFINITION yz35h10.81 Morton Fetal Cochlea Homo sapiens CDNA clone
IMAGE:285091 3', mRNA sequence.

KEYWORDS	EST.	ORGANISM
SOURCE	Homo sapiens (human)	
ORGANISM	Homo sapiens	

REFERENCE	AUTHORS
1 (bases 1 to 535)	Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B.,

TITLE	Generation and analysis of 280,000 human expressed sequence tags
JOURNAL	Genome Res. 6 (9), 807-828 (1996)
PUBMED	8889549
COMMENT	Contact: Wilson RK

Washington University School of Medicine
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: east@watson.wustl.edu
This clone is available royalty-free through LNTL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: ml3 -40 Forward
High quality sequence stop: 246.

FEATURES	Location/Qualifiers
source	1. .535

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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="CDB:3892208"
/db_xref="taxon:9606"
/clone="IMAGE:285091"
/feature_type="cocllea"
/dev_stage="16-22 week fetus"
/lab_host="SOLR cells (kanamycin resistant)"
/clone_1ib="Morton Fetal Coclelea"
/note="Organ: ear; Vector: pBluescript SK-; Site1: Eco
Site 2: XhoI; Reference: Genomics 23: 42-50 (1994) Clon
unidirectionally. Primer: Oligo dt. Fetal coclelea, nom
37% of inserts <0.5 kb, 56% 0.5-1.0 kb, 7% >1 kb. Uni-Z
XR Vector. Library constructed by N. Robertson, C. Mott
~5' adaptor sequence: 5' GAATTCGGACGAG 3' ~3' adaptor
sequence: 5' CTCGAGTTTTTTTTTTTTTTT 3'"

```

ORIGIN

Query Match	6.8%	Score 38.2;	DB 10;	Length 535;
Best Local Similarity	49.2%;	Pred. No. 1.7;		
Matches 97;	Conservative 0;	Mismatches 100;	Indels 0;	Gaps

Dy 156 ATACATAGTACAACCTCTAAGTTTCGTAGACTATTTTACATAAAATAGTGCTACACCGTTGT 2
||| ||| ||| ||| ||| ||| ||| ||| |||
Db 218 ATGTAATACCCTCAACACAGTTAGCTTGAATAAAAAATCAAACAAAAGCAAAAAACCATTTTT 2

Qy	216	ATAGGCTCCAAATACATACACACACATGAACCTTTTGGCAGTGCACAAAAGTACGTGC	275
Db	278	ATTGGCCCAATTCAACAGGTTTACTTAAAAATTGACTTATGGGTAAATACAGGC	337
Qy	276	GGCAGTACAGTAAGGCGGCTTATCGGGTGCCTCTGCACGTAACGAATACATTACG	335
Db	338	TCCATTCGGTAACCAACTTGGCATGGTTTACTACACACTGGACCAAGGTTTAG	397
Qy	336	GACCGACGAGTGTGT	352
Db	398	GACGAGATAATATTT	414

RESULT 8

LOCUS	BZ902838	578 bp	DNA	linear	GSS 12-JUN-2003
DEFINITION	CH240_23B3.TJ CHORI-240 Bos taurus genomic clone CH240_23B3,				
	genomic survey sequence.				

KEYWORDS	GSS.
SOURCE	Bos taurus (cattle)
ORGANISM	Bos taurus

REFERENCE
AUTHORS
1 (bases 1 to 578)
Larkin, D.M., Everts-van der Wind, A., Rebeiz, M., Schweitzer, P.A.,

JOURNAL	genome sequence
PUBMED	Genome Res. 13 (8), 1966-1972 (2003)
COMMENT	12902387
	Other GSSs: CH240_23B3.TV

Contact: Harris Lewin
Department of Animal Sciences
University of Illinois at Urbana Champaign
1201 W. Gregory Dr., Urbana, IL 61801, USA
Tel: 217 313 5998
Fax: 217 244 5617
Email: h-lewin@uiuc.edu

Clones are derived from the bovine BAC library CHORI-240
(<http://www.chori.org/bacpac/bovine240.htm>). For BAC library
availability, please contact Pieter de Jong (pedejong@gmail.com).
Clones may be purchased from BACPAC Resources
(<http://www.chori.org/bacpac/ordering/information.htm>). This work
was undertaken as part of the International Bovine BAC Mapping
Consortium (IBMC) by the University of Illinois at Urbana
Champaign, USA with funds provided by Grant No. AG020-334480-11828
from USDA-CRRES and AG99-35505-8534 from USDA/NRI (Livestock
Genome Sequencing Initiative)

Plate: 23 row: B column: 3

Seq primer: SP6

Class: BAC ends.

FEATURES	Location/Qualifiers
SOURCE	1. .578

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/organism="Bos taurus"
/mol_type="genomic DNA"
/strain="bred: Hereford"
/db_xref="taxon:9913"
/clones="CH240_23B3"
/sex="Male"
/cell_type="blood"
/clone_id="CHOR1-240"
/ncbi_vector="PIRABAC1.3, Site_1: MboI, Site_2: MboI,
Hereford bull Li Domino 99375; CHOR1-240 Bovine BAC
library (Male) produced by Piter de Jong"

```

ORIGIN

Query Match	6.7%;	Score 38;	DB 12;	Length 578;
Best Local Similarity	55.2%;	Pred. No. 2.1;		

Matches 74; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

QY 1 CATGATGATAACATGATGATGCTAATGTTGCTTCAACAACAACTTCTGTGAACGTG 60
 DB 252 CAGCTGATCAATGAGCATTAAGATTAATGTTGTTATAGACACATTTGTGGAATGTA 193
 QY 61 TTTTCATGTTTGGCCAAAGACCTTTATACTCGGTGGCCCTCCACACCAACCTTTT 120
 DB 192 TTTTACCAAGCTTTTAAACACCACTTTATGTTTGGGCTTAATCATCAGCAATGAAT 133
 QY 121 GCACTGCAAAAAA 134
 DB 132 TCAGCATTAATAA 119

RESULT 9
 BZ899636 582 bp DNA linear GSS 12-JUN-2003
 LOCUS CH240.16P5.TV CHORI-240 Bos taurus genomic clone CH240.16P5,
 DEFINITION genomic survey sequence.
 ACCESSION BZ899636
 VERSION BZ899636.1 GI:31624687
 KEYWORDS GSS.
 SOURCE Bos taurus (cattle)
 ORGANISM Bos taurus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
 Pecora; Bovidae; Bovinae; Bos.
 1 (bases 1 to 582)
 Larkin,D.M., Everte-van der Wind,A., Rebeiz,M., Schweitzer,P.A.,
 Bachman,S., Green,C., Wright,C.L., Campos,E.J., Benson,L.D.,
 Edwards,J., Liu,L., Osoegawa,K., Womack,J.E., de Jong,P.J. and
 Lewin,H.A.
 A cattle-human comparative map built with cattle BAC-ends and human
 genome sequence
 Genome Res. 13 (8), 1966-1972 (2003)
 12902387
 JOURNAL
 PUBMED
 COMMENT Contact: Harris Lewin
 Department of Animal Sciences
 University of Illinois at Urbana Champaign
 1201 W. Gregory Dr., Urbana, IL 61801, USA
 Tel: 217 333 5998
 Fax: 217 244 5617
 Email: h-lewin@uiuc.edu
 Clones are derived from the bovine BAC library CHORI-240
 (http://www.chori.org/bacpac/bovine240.htm). For BAC library
 availability, please contact Pieter de Jong (pdejong@mail.cho.org).
 Clones may be purchased from BACPAC Resources
 (http://www.chori.org/bacpac/ordering/information.htm). This work
 was undertaken as part of the International Bovine BAC Mapping
 Consortium (IBMC) by the University of Illinois at Urbana
 Champaign, USA with funds provided by grant No. AG202-34480-11828
 from USDA-CSREBS and AG99-35205-8534 from USDA/NRI (Livestock
 Genome Sequencing Initiative)
 Plate: 16 row: P column: 5
 Seq primer: T7
 Class: BAC ends.

FEATURES
 source
 1..582
 Location/Qualifiers
 /organism="Bos taurus"
 /mol_type="genomic DNA"
 /strain="breed: Hereford"
 /db_xref="taxon:9913"
 /clone="CH240.16P5"
 /sex="Male"
 /cell_type="Blood"
 /clone_lib="CHORI-240"
 /note="Vector: pTAPBAC1.3; Site 1: MboI; Site 2: MboI;
 Hereford bull LI Domino 99375; CHORI-240 Bovine BAC
 library (Male) produced by Pieter de Jong"

ORIGIN
 Query Match 6.7%; Score 38; DB 12; Length 582;

Best Local Similarity 55.2%; Pred. No. 2.1;

Matches 74; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

QY 1 CATGATGATAACATGATGATGCTAATGTTGCTTCAACAACAACTTCTGTGAACGTG 60
 DB 265 CAGCTGATCAATGAGCATTAAGATTAATGTTGTTATAGACACATTTGTGGAATGTA 324
 QY 61 TTTTCATGTTTGGCCAAAGACCTTTATACTCGGTGGCCCTCCACACCAACCTTTT 120
 DB 325 TTTTACCAAGCTTTTAAACACCACTTTATGTTTGGGCTTAATCATCAGCAATGAAT 384
 QY 121 GCACTGCAAAAAA 134
 DB 385 TCAGCATTAATAA 398

RESULT 10
 DX064229 593 bp DNA linear GSS 10-JAN-2006
 LOCUS KBRB071K09F KBrB, Brassica rapa BamHI BAC library Brassica rapa
 DEFINITION subsp. pekinensis genomic clone KBRB071K09, genomic survey
 sequence.
 ACCESSION DX064229
 VERSION DX064229.1 GI:84758525
 KEYWORDS GSS.
 SOURCE Brassica rapa subsp. pekinensis
 ORGANISM Brassica rapa subsp. pekinensis
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 rosids; eustosida II; Brassicales; Brassicaceae; Brassica.
 1 (bases 1 to 593)
 Yang,T.U., Kwon,S.J., Kim,J.A., Kim,J.S., Lim,K.B., Jin,M.,
 Park,J.Y., Lim,M.H., Kim,H.I., Choi,B.S., Seol,Y.J., Park,D.S.,
 Hahn,J.H. and Park,B.S.
 End sequence of Brassica rapa BamHI (KBrB) BAC clone
 Unpublished (2005)
 Contact: Beom-Seok Park
 Brassica Genomics Team
 National Institute of Agricultural Biotechnology
 225 Seodun-Dong, Suwon, 441-707, Korea
 Tel: +82-31-299-1670
 Fax: +82-31-299-1672
 Email: pbeom@da.go.kr
 BAC end sequence of Brassica rapa ssp. pekinensis BamHI BAC clone
 KBRB071K09
 Seq primer: T7
 Class: BAC ends.

FEATURES
 source
 1..593
 Location/Qualifiers
 /organism="Brassica rapa subsp. pekinensis"
 /mol_type="genomic DNA"
 /cultivar="Chifu"
 /sub_species="pekinensis"
 /db_xref="taxon:51351"
 /clone="KBRB071K09"
 /lab_host="E.coli DH10B"
 /clone_lib="KBrB, Brassica rapa BamHI BAC library"
 /note="Vector: pCUGIBAC1; Site 1: BamHI; Brassica rapa ssp
 pekinensis var. Chifu BAC library (KBrB BAC) is provided
 by Yong-Pyo Lim (CNU)."

ORIGIN
 Query Match 6.7%; Score 37.6; DB 14; Length 593;
 Best Local Similarity 51.2%; Pred. No. 2.8;
 Matches 88; Conservative 0; Mismatches 84; Indels 0; Gaps 0;

QY 101 TCCGACACCAACTTTTGGACATGCAAAAAAAGCGTTTGACCGGGCCCATACA 160
 DB 39 TCCACCAATCAATTAAGTTCGTCGCAAAATAGAAATCGAATATGATGATGCGCAAAATA 98
 QY 161 TAGTACAACTACGTTTGTAGACTATTTTACATTAATAGTCTACCGGTGTATAG 220
 DB 99 CGATTTCAACTTAATATTAATTAAGAAAAAAGTACAAATTTTTTAAAGGTATAAT 158

QY 221 CTCGAAATACATACACACATTCGCTTTTTCAGTCGCAAAAAGTACGT 272
 Db 159 CTACATTGACTATTAACAGAAATTAATCAATTAATTAACAGATTAACGACGT 210

RESULT 11
 CB410241 425 bp mRNA linear EST 24-MAR-2003
 LOCUS CB410241
 DEFINITION NISC.nci0d09.x1 COGENE 6E MAX Homo sapiens cDNA clone IMAGE:5776553
 3', mRNA sequence.

ACCESSION CB410241
 VERSION CB410241.1 GI:2916981
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homiidae; Homo.
 1 (bases 1 to 425)
 NCI-CCGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index

JOURNAL Unpublished (1997)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgaaps-r@mail.nih.gov
 CDNA Library Preparation: CDNA Library Arrayed by: The I.M.A.G.E. Consortium/LLNL
 DNA Sequencing by: National Institutes of Health Intramural
 Sequencing Center (NISC)
 Clone distribution: NCI-CCGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 info@image.llnl.gov
 Plate: LHAM12849 row: G column: 18
 Seq primer: -21M13 forward primer (ABI).
 Location/Qualifiers

FEATURES
 source
 1..425

/organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:5776553"
 /cissue_type="maxilla, pooled"
 /dev_stage="6 weeks postconception"
 /lab_host="DH10B"
 /clone_lib="COGENE 6E MAX"
 /note="Vector: PAMP1; CDNA primed using oligo-dT primer,
 directionally cloned into UDG sites of PAMP1. Size
 selected for insert sizes ranging from 0.2-1.8 kb.
 Normalized to Cot5. Primary library, non-amplified.
 Library constructed by M. Lovett. For more information on
 this library, please contact R. Tidwell (Washington
 University) or visit the COGENE website at
 http://hg.wustl.edu/COGENE/."

ORIGIN

Query Match 6.6%; Score 37.2; DB 4; Length 425;
 Best Local Similarity 54.3%; Pred. No. 3.4;
 Matches 75; Conservative 0; Mismatches 63; Indels 0; Gaps 0;

QY 115 TTTTTCAGCTGCAAAAAACAGCTTTTTCAGCGGGCCATACATAGTACAACTCTA 174
 Db 66 TTTTTCGAAAAAGAAAAAATTTTTCCTCGGGTTTATTCACATGTCATATAGTGA 125
 QY 175 CGTTGTGATGACATTTTATATATAATAGTCTACACCTGTATACGCTCCAAATACCTA 234
 Db 126 TTTTATGCAATATATATTTGCCAAAAAAGCTGAGCTTTTATTTTCCATTTTAAACACTA 185
 QY 235 CCACATTCGAACCTTT 252
 Db 186 CAATATTTACAGCTGTT 203

RESULT 12

CO384338 669 bp mRNA linear EST 30-JUN-2004
 LOCUS CO384338
 DEFINITION AGENCOURT_26189343 Blumberg,Cho dorsal blastopore 1lp Xenopus
 laevis cDNA clone IMAGE:7297357 3', mRNA sequence.

ACCESSION CO384338
 VERSION CO384338.1 GI:49490161
 KEYWORDS EST.
 SOURCE Xenopus laevis (African clawed frog)
 ORGANISM Xenopus laevis

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
 Xenopodinae; Xenopus; Xenopus.
 1 (bases 1 to 669)
 NIH-MGC http://mgc.ncbi.nlm.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)

JOURNAL Contact: Daniela S. Gerhard, Ph.D.
 COMMENT Office of Cancer Genomics
 National Cancer Institute / NIH
 Bidg. 31 Rm10A07 Bethesda, MD 20892
 Email: cgaaps-r@mail.nih.gov
 Tissue Procurement: Bruce Blumberg
 CDNA Library Preparation: B. Blumberg
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LHAM15322 row: J column: 11
 High quality sequence stop: 534.
 Location/Qualifiers

FEATURES
 source
 1..669

/organism="Xenopus laevis"
 /mol_type="mRNA"
 /db_xref="taxon:8355"
 /clone="IMAGE:7297357"
 /sex="both"
 /cissue_type="dorsal blastopore 1lp"
 /lab_host="TOP10"
 /clone_lib="Blumberg,Cho dorsal blastopore 1lp"
 /note="Organ: embryo; Vector: pluescript SK-; Site: 1:
 EcoRI; Site 2: XhoI; Library was prepared from 50 ug of
 total RNA by oligo-dT priming and AMV reverse
 transcriptase. After addition of EcoRI linker and
 EcoRI-XhoI digestion, the cDNA was size selected by
 chromatography on Sepharose CL-4B columns and firections
 containing cDNAs larger than 500 bp were ligated into
 EcoRI-XhoI-digested lambda ZAPII (Unizp-XR) and packaged
 in vitro. Average insert size is 1.4 kb. The original
 library contained 6 x 10⁶ recombinants, of which 3 x 10⁶
 were amplified and stored at -70 C in SM buffer containing
 7% DMSO. 3 x 10⁶ pfu were mass excised and the resulting
 phagemids used to infect Top10. References: Science 253,
 196-196 and Methods in Molecular Biology 97, 555-574.
 Additional sequences from this library have been deposited
 under the name Xenopus laevis dorsal blastopore 1lp.
 Library constructed by Bruce Blumberg (University of
 California, Irvine, Department of Developmental and Cell
 Biology)."

ORIGIN

Query Match 6.6%; Score 37.2; DB 8; Length 669;
 Best Local Similarity 57.9%; Pred. No. 3.8;
 Matches 66; Conservative 0; Mismatches 48; Indels 0; Gaps 0;

QY 153 CCATATCATATGATCAAACTCTACGTTTCGTAGCATATTTTACATAAATAGTACACCGT 212
 Db 104 CCAATTAATATAGGGAACCTTTCGTATAGTTGAAGATATCATCAATGATATGCAAGCT 163
 QY 213 TGTATACGCTCCAAATACACTACACACATTTGAACCTTTTTCGACGCAAAAAA 266
 Db 164 TGTATGTCAGAAATTAATTAATCTTTTTCCTTTTTCGACGTTGAAATA 217

RESULT 13
DN873866 822 bp mRNA linear EST 21-APR-2005
LOCUS nad29c08.y1 Dog eye cornea. Unnormalized (nad) Canis familiaris
DEFINITION cDNA clone nad29c08 5', mRNA sequence.
ACCESSION DN873866
VERSION DN873866.1 GI:62843807
KEYWORDS EST.
SOURCE Canis familiaris (dog)
ORGANISM Canis familiaris
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
Canis.

REFERENCE
AUTHORS Wistow, G.
TITLE NEIBank analysis of Dog cornea
JOURNAL Unpublished (2005)
COMMENT Contact: Wistow G
Section on Molecular Structure and Function
National Eye Institute
6/31, NIH, Bethesda, MD 20892-2740, USA
Tel: 301 402 3452
Fax: 301 496 0078
Email: Graeme@helix.nih.gov
Plate: 29 row: c column: 08
Seq primer: Universal M13 Reverse.
Location/Qualifiers
1. 822
/organism="Canis familiaris"
/mol_type="mRNA"
/strain="Beagle"
/db_xref="taxon:9615"
/clone="nad29c08"
/issue_type="Cornea"
/dev_stage="Adult"
/lab_host="EMDH10B"
/clone_lib="Dog eye cornea. Unnormalized (nad)"
/note="Organ: Eye; Vector: pCMVSPORT6; RNA was extracted from dog cornea tissue. A directionally cloned cDNA library in the pCMVSPORT6 vector (Invitrogen) was constructed at Bioseres Biotechnology (Laurel MD) essentially following the protocols of the SuperScript Plasmid System, full details of which are contained in the manufacturer's instruction manual (http://www.lifetechn.com/). First strand synthesis was carried out using a Not I primer-adaptor [5'-pGCTAGTCTAGATCGAGCGCGCCG(T)15-3']. cDNA was cloned in Not I/Sal I sites. EST analysis was performed at the NIH Intramural Sequencing Center (NISC). Analyzed data available through http://neibank.nih.gov."

ORIGIN
Query Match 6.6%; Score 37; DB 9; Length 822;
Best Local Similarity 50.3%; Pred. No. 4.7;
Matches 91; Conservative 0; Mismatches 90; Indels 0; Gaps 0;

QY 315 CACGTAAGATCAATATTGACCGGACGAGTGTGTTCTTATCGTACAGACGCCAGC 374
DB 33 CCGGAGCGGCGCGGACCGGAGCCCGGAGCCGAGCGCGCGCGGCGAGCGCGCAGA 92
QY 375 TTCTGTGTTGCTAAACCGGACCGGACGCAATCTCTTATGGAACAGAGAGCGCTTCAT 434
DB 93 TAACTGTGCCCCGAAACCGCGCGCTGCGCCCTCCCGCGCGCGCTCCCGGACTT 152
QY 435 ATGAGCGCGCGTATATCTCATGCGCGTGAACGAGACAGAGCGCGCTCCCGCTTATCGC 494
DB 153 CTCGCGTCCGAGCTCTCAGAGCGCGCGGAGTCTCTTGACCGGATTCCTCAAGATTCGCCG 212
QY 495 G 495
DB 213 G 213

RESULT 14
CV918268/c 576 bp mRNA linear EST 25-JAN-2005
LOCUS PH00SH10 cyets, germinating Phytophthora infestans cDNA, mRNA
DEFINITION sequence.
ACCESSION CV918268
VERSION CV918268.1 GI:58107817
KEYWORDS EST.
SOURCE Phytophthora infestans (potato late blight agent)
ORGANISM Phytophthora infestans
Eukaryota; stramenopiles; Oomycetes; Peronosporales; Phytophthora.

REFERENCE
AUTHORS Randall, T., Dwyer, R.A., Huitema, E., Beyer, K., Cytanich, C., Kelkar, H., Fong, A.M., Gates, K., Roberts, S., Yazdkan, E., Gaffney, T., Law, M., Testa, A., Torro-Alalibo, A., Zhang, M., Zheng, L., Mueller, E., Windass, J., Binder, A., Birch, P.R.J., Gisi, U., Govers, F., Gow, N.A., Mauch, F., van West, P., Maugh, M.E., Yu, J., Bolter, T., Kamoun, S., Lam, S.T. and Judelson, H.S.
TITLE Large-scale gene discovery in the oomycete phytophthora infestans reveals likely components of phytopathogenicity shared with true fungi
JOURNAL Mol. Plant-Microbe Interact. 18 (3), 229-243 (2005)
PUBMED 15782637
COMMENT Contact: Judelson HS
Department of Plant Pathology
University of California
Webber Hall, Riverside, CA 92521, USA
Tel: 909 787 4199
Fax: 909 787 4294
Email: howard.judelson@ucr.edu.
Location/Qualifiers
1. 576
/organism="Phytophthora infestans"
/mol_type="mRNA"
/strain="88069"
/db_xref="taxon:4787"
/sex="A1"
/clone_lib="cyets, germinating"
/note="Vector: pSPORT1"

ORIGIN
Query Match 6.5%; Score 36.8; DB 8; Length 576;
Best Local Similarity 55.1%; Pred. No. 5;
Matches 65; Conservative 0; Mismatches 53; Indels 0; Gaps 0;

QY 8 ATAAACAATGTATGTGCTATATGTTGCTTCAACAACAATCTGTGAAGTGTTCAT 67
DB 494 AAAAAAAAAAANANANANNTTGTTCATGAAAACTTTTGTCAAAATTACATACTAT 435
QY 68 GTTTGCCAACAGCACTTTATATCTCGGTGCGCTCCCAACCAACAATTTTGGACT 125
DB 434 GTGTATCAGACCAACACATCTCCGCGCTGCTGCTGCAGTAGATTTTGGACT 377

RESULT 15
CNS0039X/c 1101 bp DNA linear GSS 03-JUN-1999
LOCUS Drosophila melanogaster genome survey sequence T7 end of BAC #
DEFINITION BACR08012 of RCI-98 library from Drosophila melanogaster (fruit fly) genomic survey sequence.
ACCESSION CNS0039X
VERSION AL063938.1 GI:4941795
KEYWORDS GSS.
SOURCE Drosophila melanogaster (fruit fly)
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Spinharioidea; Drosophilidae; Drosophila.
REFERENCE
AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :

COMMENT

BP 191 91006 EVRY cedex - FRANCE (E-mail : segete@genoscope.cns.fr
 - Web : www.genoscope.cns.fr)
 Determination of this BAC-end sequence was carried out as part of a
 collaboration with the Berkeley Drosophila Genome Project (BDGP).
 The BDGP is constructing a physical map of the Drosophila
 melanogaster genome using these BACs. For further information
 please see [http://www.fruitfly.org/TheBDGP/Drosophila](http://www.fruitfly.org/TheBDGP/Drosophila%20melanogaster%20BAC%20library.html)
 melanogaster BAC library was prepared by Kazuo Ooegawa and
 Aaron Mammmer in Pieter de Jong's laboratory in the Department of
 Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
 NY. The library is named RPCI-98 and was constructed by partial
 EcoRI digestion of Drosophila DNA provided by the BDGP from the
 isogenic strain Y2; cn bw sp. the same strain used for the BDGP's
 pl and EST libraries. A more detailed description of the library
 and how to order individual BAC clones, the entire library, or
 filters for hybridization from the BACPAC Resource Center can be
 found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.

FEATURES

source
 1. 1101
 /organism="Drosophila melanogaster"
 /mol_type="genomic DNA"
 /db_xref="taxon:7227"
 /clone="BACR08012"
 /clone_lib="RPCI-98"
 /note="end : T7"

ORIGIN

Query Match 6.5%; Score 36.8; DB 14; Length 1101;
 Best Local Similarity 35.9%; Pred. No. 5.8;
 Matches 61; Conservative 35; Mismatches 74; Indels 0; Gaps 0;
 QY 73 CCAACAAGCAGCCTTTATCTGGTGGCTCCCAACGCACTTTTGCAGCAAAA 132
 Db 1068 CATTMTATTTACACACATATATCTCTCTTCTTACACAAATATWACTATWCACTMTAYA 1009
 QY 133 AACACGCTTTGACGCGGCGCCATACATAGTACAACTCTACGTTTGTAGACTATTTT 192
 Db 1008 CMCACYYAWCACAAMCMTCCCTCTCTATATAACATCTAATAATCAMAAYTACMAH 949
 QY 193 ACATTAATAGTACACCGCTTGTATAGCTCCAATACACTACACACAT 242
 Db 948 MAMAAMAWATATWCMAYHMTTTCACACACWCACTATACWCMWACYACWT 899

Search completed: June 15, 2006, 18:15:40
 Job time : 4724.79 secs

Db 64 SRYRQWMSGKWCYCCGCGACMCTMRBMKSWYSRSKRWCMCRYMSAAYRYSK 5
Qy 486 GCTT 489
Db 4 RTKP 1

RESULT 2
US-09-148-545-89
Sequence 89, Application US/09148545
Patent No. 6590075
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: 70 Human Secreted Proteins
FILE REFERENCE: P2001P1
CURRENT APPLICATION NUMBER: US/09/148, 545
EARLIER FILING DATE: 1998-09-04
EARLIER APPLICATION NUMBER: PCT/US98/04482
EARLIER FILING DATE: 1998-03-06
EARLIER APPLICATION NUMBER: 60/040,162
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040,333
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/038,621
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040,161
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040,626
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040,334
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040,336
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040,163
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/047,615
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,600
EARLIER FILING DATE: 1997-05-23
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EARLIER FILING DATE: 1997-05-23
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EARLIER APPLICATION NUMBER: 60/047,633
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,583
EARLIER FILING DATE: 1997-05-23
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EARLIER FILING DATE: 1997-05-23
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EARLIER FILING DATE: 1997-05-23
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EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,584
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,500
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,587
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,492
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,598
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,613
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,582
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,596
EARLIER FILING DATE: 1997-05-23

EARLIER APPLICATION NUMBER: 60/047,612
EARLIER FILING DATE: 1997-05-23
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EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,601
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/043,580
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043,568
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043,314
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043,569
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043,311
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043,671
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043,674
EARLIER FILING DATE: 1997-04-11
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EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043,672
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043,315
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/048,974
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/056,886
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,877
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,889
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,893
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,630
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,878
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,662
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,872
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,882
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,637
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,903
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,888
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,879
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,880
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,894
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,911
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,636
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,874
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,910
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,864
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,631

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; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,845
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,892
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/047,595
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/057,761
; EARLIER FILING DATE: 05-Sep-1997
; EARLIER APPLICATION NUMBER: 60/047,599
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,588
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,585
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,586
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,590
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,594
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,589
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,593
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,614
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/043,578
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,576
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/047,501
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/043,670
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/056,632
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,664
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,876
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,881
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,909
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,875
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,862
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,887
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,908
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/048,964
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/057,650
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/056,884
; EARLIER FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 280
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 89
; LENGTH: 855

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Query Match 6.1%; Score 34.4; DB 3; Length 855;
Best Local Similarity 55.6%; Pred. No. 0.41;
Matches 65; Conservative 0; Mismatches 52; Indels 0; Gaps 0;

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Qy 439 GCCGCCGTTATCTCATGCGCGTACCGGACAGAGCGCGCCGCTTATCGCGCTT 498
Db 12 GCCGCACCCGAGCTCAGCTCGGCCACCCACCACTTCCAGTCCGCGCACGAGTGGCTT 71
Qy 499 ATAAATACAGCCCGCAACGATCTGTGTAACACAGTTCAGATCTGTACAGCGA 555

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Db 72 ATGCGTCCCTCACTCGGCGCTGCGACAGAGNACTTGACTGACGAGTGCAGCGA 128
RESULT 3
US-09-621-011-89
; Sequence 89, Application US/09621011
; Patent No. 6878687
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 70 Human Secreted Proteins
; FILE REFERENCE: P2001P1
; CURRENT APPLICATION NUMBER: US/09/621,011
; CURRENT FILING DATE: 2000-07-20
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 280
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 89
; LENGTH: 855
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (103)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (767)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (831)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-621-011-89

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Query Match 6.1%; Score 34.4; DB 3; Length 855;
Best Local Similarity 55.6%; Pred. No. 0.41;
Matches 65; Conservative 0; Mismatches 52; Indels 0; Gaps 0;

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Qy 439 GCCGCCGTTATCTCATGCGCGTACCGGACAGAGCGCGCCGCTTATCGCGCTT 498
Db 12 GCCGCACCCGAGCTCAGCTCGGCCACCCACCACTTCCAGTCCGCGCACGAGTGGCTT 71
Qy 499 ATAAATACAGCCCGCAACGATCTGTGTAACACAGTTCAGATCTGTACAGCGA 555
Db 72 ATGCGTCCCTCACTCGGCGCTGCGACAGAGNACTTGACTGACGAGTGCAGCGA 128
RESULT 4
US-08-693-308-1/c
; Sequence 1, Application US/08693308
; Patent No. 6447996
; GENERAL INFORMATION:
; APPLICANT: HABERT-ORTOLI, Estelle
; APPLICANT: AMIRANOFF, Brigitte
; APPLICANT: LOQUET, Isabelle
; TITLE OF INVENTION: GALANIN RECEPTOR, NUCLEIC ACIDS,
; TITLE OF INVENTION: TRANSFORMED CELLS AND USES THEREOF
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESSES:
; ADDRESSER: Rhone-Poulenc Rorer Inc.
; STREET: 500 Arcola Rd. 3C43
; CITY: Collegeville
; STATE: PA
; COUNTRY: USA
; ZIP: 19426
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/693,308
; FILING DATE:
; CLASSIFICATION: 536

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PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 94/01808
FILING DATE: 17-FEB-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/FR95/00172
FILING DATE: 14-FEB-1995
ATTORNEY/AGENT INFORMATION:
NAME: Smith Ph.D., Julie K.
REGISTRATION NUMBER: 38,619
REFERENCE/DOCKET NUMBER: ST94008-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (610)454-3839
TELEFAX: (610)454-3808
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3083 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: 787..1836
US-08-693-308-1

Query Match 6.0%; Score 33.8; DB 3; Length 3083;
Best Local Similarity 54.4%; Pred. No. 1.3;

Matches 68; Conservative 0; Mismatches 57; Indels 0; Gaps 0;

QY 10 AACCATGTATGCTGCTTAATGTTCTTCAACACAAATCTTGTAATGTTTCTATGT 69

DB 2939 AAATAATGTTGGGAAATGTTCAATTAACATCATTAACAATTTAATGAAAAAGCATGC 2880

QY 70 TTGCGAACAAGCAGCTTATATCTGGGCTGCCGCCAACAATTTTTCAGTGC 129

DB 2879 ATTGTCACAGATGATGATACCCAGATATTTTCAGTCCCATGATTTTTCAGTGCAT 2820

QY 130 AAAAA 134

DB 2819 CTADA 2815

RESULT 5
US-09-270-767-25113/c
Sequence 25113, Application US/09270767
Patent No. 6703491
GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 25113
LENGTH: 902
TYPE: DNA
ORGANISM: Drosophila melanogaster
US-09-270-767-25113

Query Match 5.9%; Score 33.2; DB 3; Length 902;
Best Local Similarity 56.4%; Pred. No. 1.1;

Matches 62; Conservative 0; Mismatches 48; Indels 0; Gaps 0;

QY 205 TACACGGTTGATACGCTCAAAATACACACATTAACCTTTTCAGTGCAGAAA 264

DB 440 TAACCTGATGTAGCATCTCCAGATACATGAGCTCATAGAACTGTTGAAAAGGAAAT 381

QY 265 AAGTAGGTGTGGCAGTCACTAGGAGCCGCTTATCGGTCGGTCTCTGT 314

DB 380 ATTCCGATCTGTCTCAGAGCGGCTGTGAAACCCGCTGCTT 331

RESULT 6
US-09-270-767-9827/c
Sequence 9827, Application US/09270767
Patent No. 6703491

GENERAL INFORMATION:

APPLICANT: Homburger et al.

TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster

FILE REFERENCE: File Reference: 7326-094

CURRENT APPLICATION NUMBER: US/09/270,767

CURRENT FILING DATE: 1999-03-17

NUMBER OF SEQ ID NOS: 62517

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 9827

LENGTH: 5003

TYPE: DNA

ORGANISM: Drosophila melanogaster

US-09-270-767-9827

Query Match 5.9%; Score 33.2; DB 3; Length 5003;
Best Local Similarity 56.4%; Pred. No. 2.7;

Matches 62; Conservative 0; Mismatches 48; Indels 0; Gaps 0;

QY 205 TACACGGTTGATACGCTCAAAATACACACATTAACCTTTTCAGTGCAGAAA 264

DB 1212 TAACCTGATGTAGCATCTCCAGATACATTAAGCTCATGAACTGTTGAAAAGGAAAT 1153

QY 265 AAGTAGGTGTGGCAGTCACTAGGCGGCTTATCGGTCGCTCTGT 314

DB 1152 ATTCCGATCTGTCTCAGAGCGGCTGTGAAACCCGCTGCTT 1103

RESULT 7
US-09-949-016-103819
Sequence 103819, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 103819
LENGTH: 601
TYPE: DNA
ORGANISM: Human
US-09-949-016-103819

Query Match 5.7%; Score 32.2; DB 3; Length 601;
Best Local Similarity 56.0%; Pred. No. 1.9;

Matches 61; Conservative 0; Mismatches 48; Indels 0; Gaps 0;

QY 7 GATAAACAATGATGCTGCTTAATGTTGCTTCAACAACAATCTGTGAACGTGTTTCA 66

DB 463 GCTAAACAATGATGATGCTGCTTCTTCTCAGAAATTAATGATGTAAGTGAATTAA 522

QY 67 TGTGGCAACAAGCAGCTTTTATCTCGGTGCGCTCCAGACCAACT 115

DB 523 TCTATCAATATGCTCTTTTCTTAATCAATGTTCCCATCTCAGATT 571

RESULT 8
US-09-949-016-103820
; Sequence 103820, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 103820
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-103820

Query Match
Best Local Similarity 56.0%; Score 32.2; DB 3; Length 601;
Pred. No. 1.9;
Matches 61; Conservative 0; Mismatches 48; Indels 0; Gaps 0;

Qy 7 GATTAACAATGATGTGCTAATGCTTCAACAACAATCTGTGAAGTGTTCCTTCA 66
Db 133 GCTAAACATGATATTTGAGACTTTCTTCAGGAATTAATGATCTGAAGTGTATTAA 192
Qy 67 TGTTCGCAACAGCACCCTTATTAATCTGGTGGCTCCCAACCAACT 115
Db 193 TCTATCAGATATGCTCTTTCTTAATCATGATGTTCCCAATCTCAGATT 241

RESULT 9
US-09-949-016-103821
; Sequence 103821, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 103821
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-103821

Query Match
Best Local Similarity 56.0%; Score 32.2; DB 3; Length 601;
Pred. No. 1.9;
Matches 61; Conservative 0; Mismatches 48; Indels 0; Gaps 0;

Qy 7 GATTAACAATGATGTGCTAATGCTTCAACAACAATCTGTGAAGTGTTCCTTCA 66
Db 102 GCTAAACATGATATTTGAGACTTTCTTCAGGAATTAATGATCTGAAGTGTATTAA 161
Qy 67 TGTTCGCAACAGCACCCTTATTAATCTGGTGGCTCCCAACCAACT 115

Db 162 TCTATCAGATATGCTCTTTCTTAATCATGATGTTCCCAATCTCAGATT 210

RESULT 10
US-09-949-016-103863
; Sequence 103863, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 103863
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-103863

Query Match
Best Local Similarity 56.0%; Score 32.2; DB 3; Length 601;
Pred. No. 1.9;
Matches 61; Conservative 0; Mismatches 48; Indels 0; Gaps 0;

Qy 7 GATTAACAATGATGTGCTAATGCTTCAACAACAATCTGTGAAGTGTTCCTTCA 66
Db 463 GCTAAACATGATATTTGAGACTTTCTTCAGGAATTAATGATCTGAAGTGTATTAA 522
Qy 67 TGTTCGCAACAGCACCCTTATTAATCTGGTGGCTCCCAACCAACT 115
Db 523 TCTATCAGATATGCTCTTTCTTAATCATGATGTTCCCAATCTCAGATT 571

RESULT 11
US-09-949-016-103864
; Sequence 103864, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 103864
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-103864

Query Match
Best Local Similarity 56.0%; Score 32.2; DB 3; Length 601;
Pred. No. 1.9;
Matches 61; Conservative 0; Mismatches 48; Indels 0; Gaps 0;

Qy 7 GATTAACAATGATGTGCTAATGCTTCAACAACAATCTGTGAAGTGTTCCTTCA 66
Db 133 GCTAAACATGATATTTGAGACTTTCTTCAGGAATTAATGATCTGAAGTGTATTAA 192

Qy 67 TGTTCGCAACAGCAGCCTTTATCTGCGTGGCTCCGCCACCACT 115
Db 193 TCTATCAGATATGCTCTTTCTAATCCATGTTCCCATCTCAGATT 241

RESULT 12

US-09-949-016-103865
; Sequence 103865, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 103865
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-103865

Query Match 5.7%; Score 32.2; DB 3; Length 601;
Best Local Similarity 56.0%; Pred. No. 1.9;
Matches 61; Conservative 0; Mismatches 48; Indels 0; Gaps 0;

Qy 7 GATTAACATGTATGCTGCTAATGTTCTTCACACAACTTGTGAAGTGTTC 66
Db 102 GCTAAACATGATATTTGAGACTTTTCTTCAGAAATATGATCTGAAGTTGATTTAA 161
Qy 67 TGTTCGCAACAGCAGCCTTTATCTGCGTGGCTCCGCCACCACT 115
Db 162 TCTATCAGATATGCTCTTTCTAATCCATGTTCCCATCTCAGATT 210

RESULT 13

US-09-949-016-160230
; Sequence 160230, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 160230
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-160230

Query Match 5.7%; Score 32.2; DB 3; Length 601;
Best Local Similarity 56.0%; Pred. No. 1.9;
Matches 61; Conservative 0; Mismatches 48; Indels 0; Gaps 0;

Qy 7 GATTAACATGTATGCTGCTAATGTTCTTCACACAACTTGTGAAGTGTTC 66
Db 463 GCTAAACATGATATTTGAGACTTTTCTTCAGAAATATGATCTGAAGTTGATTTAA 522
Qy 67 TGTTCGCAACAGCAGCCTTTATCTGCGTGGCTCCGCCACCACT 115
Db 523 TCTATCAGATATGCTCTTTCTAATCCATGTTCCCATCTCAGATT 571

RESULT 14

US-09-949-016-160231
; Sequence 160231, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 160231
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-160231

Query Match 5.7%; Score 32.2; DB 3; Length 601;
Best Local Similarity 56.0%; Pred. No. 1.9;
Matches 61; Conservative 0; Mismatches 48; Indels 0; Gaps 0;

Qy 7 GATTAACATGTATGCTGCTAATGTTCTTCACACAACTTGTGAAGTGTTC 66
Db 133 GCTAAACATGATATTTGAGACTTTTCTTCAGAAATATGATCTGAAGTTGATTTAA 192
Qy 67 TGTTCGCAACAGCAGCCTTTATCTGCGTGGCTCCGCCACCACT 115
Db 193 TCTATCAGATATGCTCTTTCTAATCCATGTTCCCATCTCAGATT 241

RESULT 15

US-09-949-016-160232
; Sequence 160232, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 160232
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-160232

Query Match 5.7%; Score 32.2; DB 3; Length 601;

Best Local Similarity 56.0%; Pred. No. 1.9;
Matches 61; Conservative 0; Mismatches 48; Indels 0; Gaps 0;

QY	7	GATTAACAAATGTATGTGCTAATGTGCTTGCACACAAATTCTGTGAACTGTGTTTCA	66
Db	102	GCTAAACATAGATATTTGAGACTTTTCTTCAGGAATTAATGATCTGAAGTTGTATTTAA	161
QY	67	TGTTTGCCACAAACCACTTTATCTGGGTGGCTCCCCACCACT	115
Db	162	TCTATCAGAAATAGCTCTTTCTAATCAATGTTCCCCAATCTCAGATT	210

Search completed: June 15, 2006, 17:18:09
Job time : 195.328 secs

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2:	/EMC_Celerra_SIDS3/prodataa/2/pubpna/US10_PUBCOMB.seq.*	
3:	/EMC_Celerra_SIDS3/prodataa/2/pubpna/US09A_PUBCOMB.seq.*	
4:	/EMC_Celerra_SIDS3/prodataa/2/pubpna/US09B_PUBCOMB.seq.*	
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6:	/EMC_Celerra_SIDS3/prodataa/2/pubpna/US10A_PUBCOMB.seq.*	
7:	/EMC_Celerra_SIDS3/prodataa/2/pubpna/US10B_PUBCOMB.seq.*	
8:	/EMC_Celerra_SIDS3/prodataa/2/pubpna/US10C_PUBCOMB.seq.*	
9:	/EMC_Celerra_SIDS3/prodataa/2/pubpna/US10D_PUBCOMB.seq.*	
10:	/EMC_Celerra_SIDS3/prodataa/2/pubpna/US10E_PUBCOMB.seq.*	
11:	/EMC_Celerra_SIDS3/prodataa/2/pubpna/US10F_PUBCOMB.seq.*	
12:	/EMC_Celerra_SIDS3/prodataa/2/pubpna/US10G_PUBCOMB.seq.*	
13:	/EMC_Celerra_SIDS3/prodataa/2/pubpna/US11A_PUBCOMB.seq.*	
14:	/EMC_Celerra_SIDS3/prodataa/2/pubpna/US11B_PUBCOMB.seq.*	
15:	/EMC_Celerra_SIDS3/prodataa/2/pubpna/US11C_PUBCOMB.seq.*	
16:	/EMC_Celerra_SIDS3/prodataa/2/pubpna/US11D_PUBCOMB.seq.*	

Result No.	Query Score	Match Length	DB ID	Description
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1	564	100.0	564	3	US-09-896-888A-1	Sequence 1, Appl
2	548	97.2	560	9	US-10-622-088-136	Sequence 126, App
3	548	97.2	2773	7	US-10-295-074-60	Sequence 60, Appl
4	548	97.2	2773	9	US-10-846-911-60	Sequence 60, Appl
5	548	97.2	2773	10	US-10-939-107-60	Sequence 60, Appl
6	546.4	96.9	5038	9	US-10-622-088-89	Sequence 89, Appl
7	462	81.0	462	3	US-09-896-888A-14	Sequence 14, Appl
8	62	11.0	147	9	US-10-622-088-127	Sequence 127, App
9	62	11.0	325	9	US-10-622-088-149	Sequence 149, App
10	57	10.1	92	3	US-09-896-888A-16	Sequence 16, Appl
11	42.6	7.6	88	3	US-09-896-888A-15	Sequence 15, Appl
12	39.6	7.0	6289	9	US-10-473-126-139	Sequence 199, Appl
13	39.6	7.0	6289	8	US-10-423-717A-23	Sequence 223, App
14	38	6.7	6289	9	US-10-473-126-134	Sequence 345, App
15	35.4	6.3	986	8	US-10-398-224-1528	Sequence 1528, App
16	35.4	6.3	1549	8	US-10-398-224-3152	Sequence 3152, App
17	34.4	6.1	855	3	US-09-981-876-89	Sequence 89, Appl

18	-34.4	6.1	855	3	US-09-148-545-89	Sequence 89, App1
19	34.4	6.1	855	10	US-10-979-111-89	Sequence 89, App1
C 20	34.2	6.1	436	9	US-10-425-115-104158	Sequence 104158, App1
C 21	34	6.0	18977	13	US-11-067-153-26311	Sequence 26311, App1
C 22	33.8	6.0	600	13	US-11-060-756-2178	Sequence 2178, App1
C 23	33.8	6.0	600	13	US-11-060-756-2179	Sequence 2179, App1
C 24	33.8	6.0	600	13	US-11-060-756-6450	Sequence 6450, App1
C 25	33.8	6.0	600	13	US-11-060-756-6451	Sequence 6451, App1
C 26	33.8	6.0	930	4	US-09-925-065A-27884	Sequence 27884, App1
C 27	33.8	6.0	930	5	US-09-925-065A-27884	Sequence 27884, App1
C 28	33.8	6.0	930	12	US-10-301-480-129121	Sequence 129121, App1
C 29	33.8	6.0	930	12	US-10-301-480-142530	Sequence 142530, App1
C 30	33.8	6.0	126	4	US-09-925-065A-68947	Sequence 68947, App1
C 31	33.8	6.0	126	5	US-09-925-065A-68947	Sequence 68947, App1
C 32	33.8	6.0	126	12	US-10-301-480-170186	Sequence 170186, App1
C 33	33.8	6.0	126	12	US-10-301-480-783595	Sequence 783595, App1
C 34	33.8	6.0	2117	6	US-10-087-192-1463	Sequence 1463, App1
C 35	33.8	6.0	3056	6	US-10-225-567A-125	Sequence 125, App1
C 36	33.8	6.0	3083	7	US-10-166-568-1	Sequence 1, App1
C 37	33.8	6.0	39344	6	US-10-087-192-1462	Sequence 1462, App1
C 38	33.2	5.9	573	4	US-09-925-065A-559402	Sequence 559402, App1
C 39	33.2	5.9	573	5	US-09-925-065A-559402	Sequence 559402, App1
C 40	33.2	5.9	621	8	US-10-437-963-77138	Sequence 77138, App1
C 41	33	5.9	14429	8	US-10-311-455-2215	Sequence 2215, App1
C 42	33	5.9	14429	7	US-10-433-793-127	Sequence 127, App1
C 43	32.8	5.8	426	10	US-10-779-543-9174	Sequence 9174, App1
C 44	32.8	5.8	454	3	US-09-770-444-580	Sequence 580, App1
C 45	32.8	5.8	2000	3	US-09-938-842A-5148	Sequence 5148, App1

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US-09-896-888A-1
Sequence 3
US-09-896-888A-1
Sequence 1, Application US/09896888A
Patent No. US20020116723A1
GENERAL INFORMATION:
APPLICANT: The University of British Columbia
TITLE OF INVENTION: Insect Expression Vectors
FILE REFERENCE: 80021-44
CURRENT APPLICATION NUMBER: US/09/896, 888A
CURRENT FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: US/09/048, 911
PRIOR FILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: 60/049, 946
PRIOR FILING DATE: 1997-03-27
NUMBER OF SEQ ID NOS: 50
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 564
TYPE: DNA
ORGANISM: Oxyria pseudotsugata
US-09-896-888A-1

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100.08; Score 564; DB 3; Length 564;
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Best Local Similarity 100.0%; Pred. NO. 4.8E-1/5;
Matches 564; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	CATGATGATAAACAAATGTAATGCGTAATGTTGCTCAACAACAATCTGTTGAACGTG	60
Db	1	CATGATGATAAACAAATGTAATGCGTAATGTTGCTCAACAACAATCTGTTGAACGTG	60
Qy	61	TTTTCAATGTTTGCCAAAGACCTTTATTACTCGGTGGCTCCCAACCAACCACTTTT	120
Db	61	TTTTCAATGTTTGCCAAAGACCTTTATTACTCGGTGGCTCCCAACCAACCACTTTT	120
Qy	121	GCACTGCAAAAAACACGCTTTTGACCGGGGCCATCATAGTAACAACTCTACGTTTC	180
Db	121	GCACTGCAAAAAACACGCTTTTGACCGGGGCCATCATAGTAACAACTCTACGTTTC	180
Qy	181	GTAGACTATTTTACATAAATAGCTTACACCGTTGTAATAGCTCCAAATACATACGAC	240

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Db 181 GTAGACTATTATTAATAATAGTCTACACCGTGTATACGCTCCAAATACACTACACAC 240
Qy 241 ATTGAACCTTTTTCAGTGCAGAAAAAGTACGTGTGCGGCACTCAGTATAGCGGGCTTATC 300
Db 241 ATTGAACCTTTTTCAGTGCAGAAAAAGTACGTGTGCGGCACTCAGTATAGCGGGCTTATC 300
Qy 301 GGGTCGGCTCTGTCACTAGCAATCACTATTCGAGACCGGACGAGTGTGTCTTATCGT 360
Db 301 GGGTCGGCTCTGTCACTAGCAATCACTATTCGAGACCGGACGAGTGTGTCTTATCGT 360
Qy 361 GACAGACGCCAGCTTCTGTGTCTTAAACCGGACCGGAGCACTCTTATCGAACA 420
Db 361 GACAGACGCCAGCTTCTGTGTCTTAAACCGGACCGGAGCACTCTTATCGAACA 420
Qy 421 GGAGCGCCCTTCATATCAGCCGCGGCTTATCTCATGCGCGTACCGGACAGAGCGCC 480
Db 421 GGAGCGCCCTTCATATCAGCCGCGGCTTATCTCATGCGCGTACCGGACAGAGCGCC 480
Qy 481 GTCCCGCTTATCGGCGCTTATTAATATACAGCCGCAACGATCGTAAACAGTTGAACAG 540
Db 481 GTCCCGCTTATCGGCGCTTATTAATATACAGCCGCAACGATCGTAAACAGTTGAACAG 540
Qy 541 CATCTGTACAGCAGCAACATG 564
Db 541 CATCTGTACAGCAGCAACATG 564
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RESULT 2
US-10-622-088-126
; Sequence 126, Application US/10622088
; Publication No. US20040219516A1
; GENERAL INFORMATION:
; APPLICANT: Bennett, Robert P.
; APPLICANT: Welch, Peter J.
; APPLICANT: Harwood, Steven
; APPLICANT: Madden, Knut
; APPLICANT: Frimpong, Kenneth
; APPLICANT: Franke, Kenneth E.
; TITLE OF INVENTION: Viral Vectors Containing Recombination Sites
; FILE REFERENCE: 0942.545007
; CURRENT APPLICATION NUMBER: US/10/622,088
; PRIOR FILING DATE: 2003-07-18
; PRIOR APPLICATION NUMBER: PCT/US03/22437
; PRIOR FILING DATE: 2003-07-18
; PRIOR APPLICATION NUMBER: US 60/396,335
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: US 60/398,617
; PRIOR FILING DATE: 2002-07-26
; PRIOR APPLICATION NUMBER: US 60/427,231
; PRIOR FILING DATE: 2002-11-19
; PRIOR APPLICATION NUMBER: US 60/456,496
; PRIOR FILING DATE: 2003-03-24
; PRIOR APPLICATION NUMBER: US 60/474,940
; PRIOR FILING DATE: 2003-06-03
; NUMBER OF SEQ ID NOS: 165
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 126
; LENGTH: 560
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: OpIE2 promoter sequence
US-10-622-088-126
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Query Match 97.2%; Score 548; DB 9; Length 560;
Best Local Similarity 100.0%; Pred. No. 9..2e-170;
Matches 548; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 CATGATATAACAATGATGCTATGCTTCAACAACAATCTGTGAACGTG 60
Db 5 CATGATATAACAATGATGCTATGCTTCAACAACAATCTGTGAACGTG 64
Qy 61 TTTTCATGTTGGCAACAGCACCCTTATTACTCGGTGCGCTCCCAACCAACTTTT 120
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Db 65 TTTTCATGTTGGCAACAGCACCCTTATTACTCGGTGCGCTCCCAACCAACTTTT 124
Qy 121 GCATCGCAAAAAACAGCTTTTGGACGCGGGCCCATACATATGATACAACTAGCTTTC 180
Db 125 GCATCGCAAAAAACAGCTTTTGGACGCGGGCCCATACATATGATACAACTAGCTTTC 184
Qy 181 GTAGACTATTATTAATAATAGTCTACACCGTGTATACGCTCCAAATACACTACACAC 240
Db 185 GTAGACTATTATTAATAATAGTCTACACCGTGTATACGCTCCAAATACACTACACAC 244
Qy 241 ATTGAACCTTTTTCAGTGCAGAAAAAGTACGTGTGCGGCACTCAGTATAGCGGGCTTATC 300
Db 245 ATTGAACCTTTTTCAGTGCAGAAAAAGTACGTGTGCGGCACTCAGTATAGCGGGCTTATC 304
Qy 301 GGGTCGGCTCTGTCACTAGCAATCACTATTCGAGACCGGACGAGTGTGTCTTATCGT 360
Db 305 GGGTCGGCTCTGTCACTAGCAATCACTATTCGAGACCGGACGAGTGTGTCTTATCGT 364
Qy 361 GACAGACGCCAGCTTCTGTGTCTTAAACCGGACCGGAGCACTCTTATCGAACA 420
Db 365 GACAGACGCCAGCTTCTGTGTCTTAAACCGGACCGGAGCACTCTTATCGAACA 424
Qy 421 GGAGCGCCCTTCATATCAGCCGCGGCTTATCTCATGCGCGTACCGGACAGAGCGCC 480
Db 425 GGAGCGCCCTTCATATCAGCCGCGGCTTATCTCATGCGCGTACCGGACAGAGCGCC 484
Qy 481 GTCCCGCTTATCGGCGCTTATTAATATACAGCCGCAACGATCGTAAACAGTTGAACAG 540
Db 485 GTCCCGCTTATCGGCGCTTATTAATATACAGCCGCAACGATCGTAAACAGTTGAACAG 544
Qy 541 CATCTGTT 548
Db 545 CATCTGTT 552
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RESULT 3
US-10-295-074-60
; Sequence 60, Application US/10295074
; Publication No. US20030185845A1
; GENERAL INFORMATION:
; APPLICANT: Pharmexa A/S
; TITLE OF INVENTION: NOVEL IMMUNOGENIC MIMETICS OF MULTIMER PROTEINS
; FILE REFERENCE: P1013DK00
; CURRENT APPLICATION NUMBER: US/10/295,074
; PRIOR FILING DATE: 2002-11-15
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 60
; LENGTH: 2773
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: p22Op2F expression vector for insect cells
; FEATURE:
; NAME/KEY: misc_recomb
; LOCATION: (561)..(566)
; OTHER INFORMATION: HindIII site
; FEATURE:
; NAME/KEY: misc_recomb
; LOCATION: (586)..(591)
; OTHER INFORMATION: EcoRI site
; FEATURE:
; NAME/KEY: misc_recomb
; LOCATION: (593)..(598)
; OTHER INFORMATION: BamHI site
; FEATURE:
; NAME/KEY: misc_recomb
; LOCATION: (625)..(630)
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Qy	1	CATATGATTAACATGATGAGTGATGATGTTGCTTCAACAACATTCGTGAACTGCG	60
Db	5	CATATGATTAACATGATGAGTGCTAATGTTGCTTCAACAACAATTCGTGAACTGCG	64
Qy	61	TTTTCATGTGTCACACAGCAACCTTTATACGTGGGCGTCCCGACCAACAATTTTT	120
Db	65	TTTTCATGTGTCACACAGCAACCTTTATACGTGGGCGTCCCGACCAACAATTTTT	124
Qy	121	GCATGCAAAAAACACGCTTTTGGACGGGGCCATACATATGTAACAACTTACGTTTC	180
Db	125	GCATGCAAAAAACACGCTTTTGGACGGGGCCATACATATGTAACAACTTACGTTTC	184
Qy	181	GTAGACTTTTTCATAATATAGTCTACACCGTTGTATAGCGTCCAAATACATACACAC	240
Db	185	GTAGACTTTTTCATAATATAGTCTACACCGTTGTATAGCGTCCAAATACATACACAC	244
Qy	241	ATTGAACCTTTTGGACGTGCAAAAAGTACGTGTGCGACGTACGTAGCGCGGCTTATC	300
Db	245	ATTGAACCTTTTGGACGTGCAAAAAGTACGTGTGCGACGTACGTAGCGCGCTTATC	304
Qy	301	GGGTGCGGCTCTGTACAGTACGAATCACTTATGGAACCGACGAGTGTGCTTATAGT	360
Db	305	GGGTGCGGCTCTGTACAGTACGAATCACTTATGGAACCGACGAGTGTGCTTATAGT	364
Qy	361	GACAGAGCGCAGCTTCTGTGTGCTTAACCGCACCGACCGACACCTCTTATCGGAACA	420
Db	365	GACAGAGCGCAGCTTCTGTGTGCTTAACCGCACCGAGCAACTCTTATCGGAACA	424
Qy	421	GGAGCGGCTCATATCAGCCGGCGGTATCTCATGCGCGTGAACCGGACAAGAGCGGCC	480
Db	425	GGAGCGGCTCATATCAGCCGGCGGTATCTCATGCGCGTGAACCGGACAAGAGCGGCC	484
Qy	481	GTCCCGCTTATCGGCGCTTAAATACAGCCGCAACGATCTGTTAAACAGTTGAACAG	540
Db	485	GTCCCGCTTATCGGCGCTTAAATACAGCCGCAACGATCTGTTAAACAGTTGAACAG	544
Qy	541	CATCTGTT 548	

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Db          545 CATCHGT 552

RESULT 4
US-10-846-911-60
Sequence 60. Application US/10846911
Publication No. US20040258660A1
GENERAL INFORMATION:
APPLICANT: KLYSNER, Steen
APPLICANT: NIELSEN, Finn Stausholm
APPLICANT: BRATT, Tomas
APPLICANT: VOLDORF, Bjorn
APPLICANT: MOURITSEN, Soren
FILE OF INVENTION: NOVEL IMMUNOGENIC MIMETICS OF MULTIMER PROTEINS
TITLE REFERENCE: 674542-2018
CURRENT APPLICATION NUMBER: US/10/846, 911
PRIORITY FILING DATE: 2004-05-14
PRIORITY APPLICATION NUMBER: PCT/DK02/00764
PRIORITY FILING DATE: 2002-11-15
PRIORITY APPLICATION NUMBER: 60/331,575
PRIORITY FILING DATE: 2001-11-16
PRIORITY APPLICATION NUMBER: PA 2001 01702
PRIORITY FILING DATE: 2001-11-16
NUMBER OF SEQ ID NOS: 60
SOFTWARE: PatentIn version 3.1
SEQ ID NO 60
LENGTH: 2773
TYPE: DNA
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: p2O2p2F expression vector for insect cells
FEATURE:
NAME/KEY: misc_recomb
LOCATION: (561)..(566)
OTHER INFORMATION: HindIII site
FEATURE:
NAME/KEY: misc_recomb
LOCATION: (573)..(578)
OTHER INFORMATION: Aval site
FEATURE:
NAME/KEY: misc_recomb
LOCATION: (586)..(591)
OTHER INFORMATION: EcoRI site
FEATURE:
NAME/KEY: misc_recomb
LOCATION: (593)..(598)
OTHER INFORMATION: BamHI site
FEATURE:
NAME/KEY: misc_recomb
LOCATION: (625)..(630)
OTHER INFORMATION: ClaI site
FEATURE:
NAME/KEY: misc_recomb
LOCATION: (629)..(634)
OTHER INFORMATION: ClaI site
FEATURE:
NAME/KEY: misc_recomb
LOCATION: (1156)..(1161)
OTHER INFORMATION: ApaLI site
FEATURE:
NAME/KEY: misc_recomb
LOCATION: (2128)..(2133)
OTHER INFORMATION: PstI site
FEATURE:
NAME/KEY: misc_recomb
LOCATION: (2204)..(2209)
OTHER INFORMATION: NcoI site
FEATURE:
NAME/KEY: misc_recomb
LOCATION: (2284)..(2289)
OTHER INFORMATION: Aval site
FEATURE:
NAME/KEY: misc_recomb

```



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Db      185 GTAGACTATTTTACATAAATAGTCTACACCGTGTATACGCTCCAAATACACTACACAC 244
Qy      241 ATTGAACCTTTTGGAGTGAAGAAAAAGTACGTCGGAGTCAGTACGGCGGCTTATC 300
Db      245 ATTGAACCTTTTGGAGTGAAGAAAAAGTACGTCGGAGTCAGTACGGCGGCTTATC 304
Qy      301 GGGTCGGCTCTGTCACTACGAATCACTATTCGACCGGACGAGTGTCTTATCGT 360
Db      305 GGGTCGGCTCTGTCACTACGAATCACTATTCGACCGGACGAGTGTCTTATCGT 364
Qy      361 GACAGACGCGACCTTCTGTGTGTCTAACCGGACCGGACGCACTCTTATCGAACA 420
Db      365 GACAGACGCGACCTTCTGTGTGTCTAACCGGACCGGACGCACTCTTATCGAACA 424
Qy      421 GGAAGCGCTCTCATATACAGCGCGGCTTATCTATCGCGCTGACCGGACGAGCGGCC 480
Db      425 GGAAGCGCTCTCATATACAGCGCGGCTTATCTATCGCGCTGACCGGACGAGCGGCC 484
Qy      481 GTCCCGCTTATCGCGCTTATTAATATACAGCGCGACGATCTGTAAACAGTGAACAG 540
Db      485 GTCCCGCTTATCGCGCTTATTAATATACAGCGCGACGATCTGTAAACAGTGAACAG 544
Qy      541 CATCTGTT 548
Db      545 CATCTGTT 552

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RESULT 6

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US-10-622-088-89
; Sequence 89, Application US/10622088
; Publication No. US20040219516A1
; GENERAL INFORMATION:
; APPLICANT: Bennett, Robert P.
; APPLICANT: Welch, Peter J.
; APPLICANT: Harwood, Steven
; APPLICANT: Madden, Knut
; APPLICANT: Frimpong, Kenneth
; APPLICANT: Frank, Kenneth E.
; TITLE OF INVENTION: Viral Vectors Containing Recombination Sites
; FILE REFERENCE: 0942.5450007
; CURRENT APPLICATION NUMBER: US/10/622,088
; PRIOR FILING DATE: 2003-07-18
; PRIOR APPLICATION NUMBER: PCT/US03/22437
; PRIOR FILING DATE: 2003-07-18
; PRIOR APPLICATION NUMBER: US 60/396,335
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: US 60/398,617
; PRIOR FILING DATE: 2002-07-26
; PRIOR APPLICATION NUMBER: US 60/427,231
; PRIOR FILING DATE: 2002-11-19
; PRIOR APPLICATION NUMBER: US 60/456,496
; PRIOR FILING DATE: 2003-03-24
; PRIOR APPLICATION NUMBER: US 60/474,940
; PRIOR FILING DATE: 2003-06-03
; NUMBER OF SEQ ID NOS: 165
; SOFTWARE: Patent version 3.2
; SEQ ID NO 89
; LENGTH: 5038
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PIB/V5-His-DEST
US-10-622-088-89

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Query Match      96.9%; Score 546.4; DB 9; Length 5038;
Best Local Similarity 99.8%; Pred. No. 9.2e-169;
Matches 547; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy      1 CAGATGATTAACAAGATGATGCTATGCTTAAACAACAATCTGTGAACGTG 60
Db      1 CAGATGATTAACAAGATGATGCTATGCTTAAACAACAATCTGTGAACGTG 60
Qy      61 TTTTCATGTTGGCAACAGACCTTATTACTCGGTGCGCTCCCAACCAACTTTT 120

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Db      61 TTTTCATGTTGGCAACAGACCTTATTACTCGGTGCGCTCCCAACCAACTTTT 120
Qy      121 GCACGTCAAAAAAACAAGCTTTTGGACGCGGGCCCATATCAATAGTACAACTTACGTTTC 180
Db      121 GCACGTCAAAAAAACAAGCTTTTGGACGCGGGCCCATATCAATAGTACAACTTACGTTTC 180
Qy      181 GTAGACTATTTTACATAAATAGTCTACACCGTGTATACGCTCCAAATACACTACACAC 240
Db      181 GTAGACTATTTTACATAAATAGTCTACACCGTGTATACGCTCCAAATACACTACACAC 240
Qy      241 ATTGAACCTTTTGGAGTGAAGAAAAAGTACGTCGGAGTCAGTACGGCGGCTTATC 300
Db      241 ATTGAACCTTTTGGAGTGAAGAAAAAGTACGTCGGAGTCAGTACGGCGGCTTATC 300
Qy      301 GGGTCGGCTCTGTCACTACGAATCACTATTCGACCGGACGAGTGTCTTATCGT 360
Db      301 GGGTCGGCTCTGTCACTACGAATCACTATTCGACCGGACGAGTGTCTTATCGT 360
Qy      361 GACAGACGCGACCTTCTGTGTGTCTAACCGGACCGGACGCACTCTTATCGAACA 420
Db      361 GACAGACGCGACCTTCTGTGTGTCTAACCGGACCGGACGCACTCTTATCGAACA 420
Qy      421 GGAAGCGCTCTCATATACAGCGCGGCTTATCTATCGCGCTGACCGGACGAGCGGCC 480
Db      421 GGAAGCGCTCTCATATACAGCGCGGCTTATCTATCGCGCTGACCGGACGAGCGGCC 480
Qy      481 GTCCCGCTTATCGCGCTTATTAATATACAGCGCGACGATCTGTAAACAGTGAACAG 540
Db      481 GTCCCGCTTATCGCGCTTATTAATATACAGCGCGACGATCTGTAAACAGTGAACAG 540
Qy      541 CATCTGTT 548
Db      541 CATCTGTT 548

```

RESULT 7

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US-09-896-888a-14
; Sequence 14, Application US/09896888A
; Patent No. US20020116723A1
; GENERAL INFORMATION:
; APPLICANT: The University of British Columbia
; TITLE OF INVENTION: Insect Expression Vectors
; FILE REFERENCE: 80021-44
; CURRENT APPLICATION NUMBER: US/09/896,888A
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US/09/048,911
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/049,946
; PRIOR FILING DATE: 1997-03-27
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: Patent Ver. 2.0
; SEQ ID NO 14
; LENGTH: 462
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Promoter
; OTHER INFORMATION: Sequence of the Opmpv 1e2 gene
US-09-896-888a-14

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Query Match      81.9%; Score 462; DB 3; Length 462;
Best Local Similarity 100.0%; Pred. No. 2.1e-141;
Matches 462; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      102 CCCACACCAACTTTTGGACCTGCAAAAAACAAGCTTTTGGACGCGGCCCATATCAT 161
Db      1 CCCACACCAACTTTTGGACCTGCAAAAAACAAGCTTTTGGACGCGGCCCATATCAT 60
Qy      162 AGTACAAACTCTACGTTTGTGTAGACTATTTTACATAAATAGTCTACACCGTGTATACGC 221
Db      61 AGTACAAACTCTACGTTTGTGTAGACTATTTTACATAAATAGTCTACACCGTGTATACGC 120

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QY 222 TCCAAATACACTACACATTAACCTTTTTCAGATGACAAAAGTACGTCGCGAGT 281
|
|
|
DB 121 TCCAAATACACTACACATTAACCTTTTTCAGATGACAAAAGTACGTCGCGAGT 180
|
|
|
QY 282 CACGTAGCGCGCTTATCGGGTCCGTCCTTTCAGCTACGAATACATTATCGGACCGG 341
|
|
|
DB 181 CAGGTAGCGCGCTTATCGGGTCCGTCCTTTCAGCTACGAATACATTATCGGACCGG 240
|
|
|
QY 342 ACAGGTGTGTCTTATGTGTGACAGAGCGCGCTTCTGTGTCTTAAACCGACCGGAC 401
|
|
|
DB 241 ACAGGTGTGTCTTATGTGTGACAGAGCGCGCTTCTGTGTCTTAAACCGACCGGAC 300
|
|
|
QY 402 GCAACTCTTATCGGAACAGAGCGCGCTCCATATCAAGCGCGTATCTATCGCGCT 461
|
|
|
DB 301 GCAACTCTTATCGGAACAGAGCGCGCTCCATATCAAGCGCGTATCTATCGCGCT 360
|
|
|
QY 462 GACCGACACGAGCGCGCTCCGCTTATCGCGCTTAAATACAGCCCGCAACGATCT 521
|
|
|
DB 361 GACCGACACGAGCGCGCTCCGCTTATCGCGCTTAAATACAGCCCGCAACGATCT 420
|
|
|
QY 522 GGTAAACAGAGTGAACAGCATCTGTAAACGCGACACAACT 563
|
|
|
DB 421 GGTAAACAGAGTGAACAGCATCTGTAAACGCGACACAACT 462
|
|
|

RESULT 8

US-10-622-088-127
; Sequence 127, Application US/10622088
; Publication No. US20040219516A1
; GENERAL INFORMATION:
; APPLICANT: Bennett, Robert P.
; APPLICANT: Welch, Peter J.
; APPLICANT: Harwood, Steven
; APPLICANT: Madden, Knut
; APPLICANT: Frippong, Kenneth
; APPLICANT: Franke, Kenneth E.
; TITLE OF INVENTION: Viral Vectors Containing Recombination Sites
; FILE REFERENCE: 0942.5450007
; CURRENT APPLICATION NUMBER: US/10/622,088
; CURRENT FILING DATE: 2003-07-18
; PRIOR APPLICATION NUMBER: PCT/US03/22437
; PRIOR FILING DATE: 2003-07-18
; PRIOR APPLICATION NUMBER: US 60/396,335
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: US 60/398,617
; PRIOR FILING DATE: 2002-07-26
; PRIOR APPLICATION NUMBER: US 60/427,231
; PRIOR FILING DATE: 2002-11-19
; PRIOR APPLICATION NUMBER: US 60/456,496
; PRIOR FILING DATE: 2003-03-24
; PRIOR APPLICATION NUMBER: US 60/474,940
; PRIOR FILING DATE: 2003-06-03
; NUMBER OF SEQ ID NOS: 165
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 127
; LENGTH: 147
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Recombination region of pIB/V5-His-DEST
; NAME/KEY: misc feature
; LOCATION: (141)..(148)
; OTHER INFORMATION: n may be any nucleotide
US-10-622-088-127

Query Match 11.0%; Score 62; DB 9; Length 147;
Best Local Similarity 100.0%; Pred. No. 1.7e-09;
Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 487 CTTATCGCGCTTAAATACAGCCCGCAAGATCTGTAAACAGATTGAACAGCATCTG 546
|
|
|
DB 1 CTTATCGCGCTTAAATACAGCCCGCAAGATCTGTAAACAGATTGAACAGCATCTG 60
|
|
|

QY 547 TT 548
|
|
DB 61 TT 62

RESULT 9

US-10-622-088-149
; Sequence 149, Application US/10622088
; Publication No. US20040219516A1
; GENERAL INFORMATION:
; APPLICANT: Bennett, Robert P.
; APPLICANT: Welch, Peter J.
; APPLICANT: Harwood, Steven
; APPLICANT: Madden, Knut
; APPLICANT: Frippong, Kenneth
; APPLICANT: Franke, Kenneth E.
; TITLE OF INVENTION: Viral Vectors Containing Recombination Sites
; FILE REFERENCE: 0942.5450007
; CURRENT APPLICATION NUMBER: US/10/622,088
; CURRENT FILING DATE: 2003-07-18
; PRIOR APPLICATION NUMBER: PCT/US03/22437
; PRIOR FILING DATE: 2003-07-18
; PRIOR APPLICATION NUMBER: US 60/396,335
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: US 60/398,617
; PRIOR FILING DATE: 2002-07-26
; PRIOR APPLICATION NUMBER: US 60/427,231
; PRIOR FILING DATE: 2002-11-19
; PRIOR APPLICATION NUMBER: US 60/456,496
; PRIOR FILING DATE: 2003-03-24
; PRIOR APPLICATION NUMBER: US 60/474,940
; PRIOR FILING DATE: 2003-06-03
; NUMBER OF SEQ ID NOS: 165
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 149
; LENGTH: 325
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Recombination region of pIB/V5 His DEST
; NAME/KEY: misc feature
; LOCATION: (141)..(142)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (145)..(276)
US-10-622-088-149

Query Match 11.0%; Score 62; DB 9; Length 325;
Best Local Similarity 100.0%; Pred. No. 2.5e-09;
Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 487 CTTATCGCGCTTAAATACAGCCCGCAAGATCTGTAAACAGATTGAACAGCATCTG 546
|
|
|
DB 1 CTTATCGCGCTTAAATACAGCCCGCAAGATCTGTAAACAGATTGAACAGCATCTG 60
|
|
|
QY 547 TT 548
|
|
DB 61 TT 62

RESULT 10

US-09-896-888a-16
; Sequence 16, Application US/09896888A
; Patent No. US20020116723A1
; GENERAL INFORMATION:
; APPLICANT: The University of British Columbia
; TITLE OF INVENTION: Insect Expression Vectors
; FILE REFERENCE: 80021-44
; CURRENT APPLICATION NUMBER: US/09/896,888A
; CURRENT FILING DATE: 2001-06-29

PRIOR APPLICATION NUMBER: US/09/048,911
PRIOR FILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: 60/049,946
PRIOR FILING DATE: 1997-03-27
NUMBER OF SEQ ID NOS: 50
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 16
LENGTH: 92
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Fragment of
OTHER INFORMATION: promoter sequence of the AcMNPV ien gene
US-09-896-888a-16

Query Match 10.1%; Score 57; DB 3; Length 92;
Best Local Similarity 77.5%; Pred. No. 5.9e-08;
Matches 69; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

Qy 186 CTAATTTACATAATAGTCTACACCGTGTATACGCTCCCAATACACTACACACATGA 245
Db 1 CTAATTTATTAATTAATCTACACTGTACATACGCTCCCAATTAATCTACTACATCA 60

Qy 246 ACCTTTTCAGTGCAGAAAAGTACGTGT 274
Db 61 ACTTTTTCATACAAAAGTTCAATT 89

RESULT 11
US-09-896-888a-15
Sequence 15, Application US/09896888A
Patent No. US20020116723A1
GENERAL INFORMATION:
APPLICANT: The University of British Columbia
TITLE OF INVENTION: Insect Expression Vectors
FILE REFERENCE: 80021-44
CURRENT APPLICATION NUMBER: US/09/896,888A
CURRENT FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: US/09/048,911
PRIOR FILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: 60/049,946
PRIOR FILING DATE: 1997-03-27
NUMBER OF SEQ ID NOS: 50
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 15
LENGTH: 88
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Fragment of
OTHER INFORMATION: promoter sequence of the AcMNPV ien gene
US-09-896-888a-15

Query Match 7.6%; Score 42.6; DB 3; Length 88;
Best Local Similarity 74.0%; Pred. No. 0.0033;
Matches 54; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

Qy 112 AACTTTTTCAGTGCAGAAAAGTGTTCACGCGGGCCCATACATAGTACAACT 171
Db 16 AATTTTTCAGATGCAAAAAGTCACTTTCCTGACACACTCATATACAGTACATCT 75

Qy 172 CTACGTTGTAG 184
Db 76 CTACAAATCGTAG 88

RESULT 12
US-10-473-126-199/C
Sequence 199, Application US/10473126
Publication No. US20040234973A1
GENERAL INFORMATION:
APPLICANT: Epigenomics AG
TITLE OF INVENTION: Methods and nucleic acids for the analysis of hematopoietic cell

TITLE OF INVENTION: proliferative disorders
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/10/473,126
CURRENT FILING DATE: 2003-09-26
NUMBER OF SEQ ID NOS: 1258
SEQ ID NO 199
LENGTH: 6289
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Chemically treated genomic DNA (Homo sapiens)
US-10-473-126-199

Query Match 7.0%; Score 39.6; DB 9; Length 6289;
Best Local Similarity 53.2%; Pred. No. 0.27;
Matches 84; Conservative 0; Mismatches 74; Indels 0; Gaps 0;

Qy 112 AACTTTTTCAGTGCAGAAAAGTGTTCACGCGGGCCCATACATAGTACAACT 171
Db 4896 AATTTATTTATTAATCAAAATTAATCTATTATTAATCCACTACAAATATCATTCAAAA 4837

Qy 172 CTACGTTGTAGACTAATTTTACATTAATAGTCTACACCGTGTATACGCTCAATACA 231
Db 4836 TAATAATTTTAAAAACATTAATTAATAAAATCGTCAATCTTTTACTCAAAAAATA 4777

Qy 232 CTACCAACATGAACTTTTTCAGTGCAGAAAAGTA 269
Db 4776 ATACAACTTCTCTCTCTATAAAAAGAAAAATA 4739

RESULT 13
US-10-221-714A-223/C
Sequence 223, Application US/10221714A
Publication No. US20040048254A1
GENERAL INFORMATION:
APPLICANT: OLEK, Alexander
APPLICANT: PIEPENBROCK, Christian
TITLE OF INVENTION: Diagnosis of Diseases Associated with
TITLE OF INVENTION: tumor suppressor genes and oncogenes
FILE REFERENCE: 5013.1005
CURRENT APPLICATION NUMBER: US/10/221,714A
CURRENT FILING DATE: 2003-01-21
PRIOR APPLICATION NUMBER: PCT/EP01/02955
PRIOR FILING DATE: 2001-03-15
PRIOR APPLICATION NUMBER: DE 10013847.0
PRIOR FILING DATE: 2000-03-15
PRIOR APPLICATION NUMBER: DE 10019058.8
PRIOR FILING DATE: 2000-04-06
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: DE 10032529.7
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 540
SEQ ID NO 223
LENGTH: 9289
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-221-714A-223

Query Match 7.0%; Score 39.6; DB 8; Length 9289;
Best Local Similarity 53.2%; Pred. No. 0.32;
Matches 84; Conservative 0; Mismatches 74; Indels 0; Gaps 0;

Qy 112 AACTTTTTCAGTGCAGAAAAGTGTTCACGCGGGCCCATACATAGTACAACT 171
Db 7896 AATTTATTTATTAATCAAAATTAATCTATTATTAATCCACTACAAATATCATTCAAAA 7837

Qy 172 CTACGTTGTAGACTAATTTTACATTAATAGTCTACACCGTGTATACGCTCAAAATACA 231

Db 7836 TAATAATTTTAAACATTAATTAATAAATCGTCAATTTCTTTACTCAAAAAATA 7777
QY 232 CTACCAACACTGAACTTTTTCAGTGCAGCAAAAAAGTA 269
Db 7776 ATACAACTTCTCTCTCCCTATMAAACGAAAAAATA 7739

RESULT 14

US-10-473-126-345/c
; Sequence 345, Application US/10473126
; Publication No. US20040234973A1
; GENERAL INFORMATION:
; APPLICANT: Epigenomics AG
; TITLE OF INVENTION: Methods and nucleic acids for the analysis of hematopoietic cell
; TITLE OF INVENTION: Proliferative disorders
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/473,126
; CURRENT FILING DATE: 2003-09-26
; NUMBER OF SEQ ID NOS: 1258
; SEQ ID NO 345
; LENGTH: 6289
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-473-126-345

Query Match 6.7%; Score 38; DB 9; Length 6289;
Best Local Similarity 52.5%; Pred. No. 0.9;
Matches 83; Conservative 0; Mismatches 75; Indels 0; Gaps 0;

QY 112 AACTTTTGCACGCAAAACACGCTTTTGACGCGGCGCATACATAGTCAAACT 171
Db 4896 AATTATTTATATACCAAAATTAACATTAATTAATCCACTACCAATATCATTCAAAA 4837
QY 172 CTACGTTTCGTAGCTATTTTACATAAATAGCTACACCGTGTATACGCTCAAAATCA 231
Db 4836 TAATAATTTTAAACATTTATTAATAAATATCATCAATTTCTTTACTCAAAAAATA 4777
QY 232 CTACCAACACTGAACTTTTTCAGTGCAGCAAAAAAGTA 269
Db 4776 ATACAACTTCTCTCTCCCTATMAAACGAAAAAATA 4739

RESULT 15

US-10-398-221-1528/c
; Sequence 1528, Application US/10398221
; Publication No. US20040018514A1
; GENERAL INFORMATION:
; APPLICANT: KUNST, Frederik
; APPLICANT: GLASER, Philippe
; TITLE OF INVENTION: Listeria innocua, genome and applications
; FILE REFERENCE: 344 702 - US
; CURRENT APPLICATION NUMBER: US/10/398,221
; CURRENT FILING DATE: 2003-03-27
; PRIOR APPLICATION NUMBER: PCT/FR 01/03 061
; PRIOR FILING DATE: 2001-10-04
; PRIOR APPLICATION NUMBER: FR 00/12 697
; NUMBER OF SEQ ID NOS: 4025
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1528
; LENGTH: 986
; TYPE: DNA
; ORGANISM: Listeria monocytogenes-4B
; FEATURE:
; NAME/KEY: misc-feature
; LOCATION: (1)..(end)
; OTHER INFORMATION: n can be any nucleotide a,g,c or t/u
US-10-398-221-1528

Query Match 6.3%; Score 35.4; DB 8; Length 986;

Best Local Similarity 56.4%; Pred. No. 2.6;
Matches 66; Conservative 0; Mismatches 51; Indels 0; Gaps 0;

QY 155 CATACATAGTACAAACTTACGTTTGTAGACTATTTTACATTAATAGTCTACACCGTG 214
Db 318 CAGATTAGAAACATTTATCGTGGCCAGAAAAATTAATCAAGAGCACTCTGTG 259
QY 215 TATACGCTCCAAATACACTACACACATTTGAGTGCAGCAAAAAAGTACG 271
Db 258 CAGAACATTCATTAAGTTACATTCATTGCTCAATTTTCGGTGTCTGAGAGAG 202

Search completed: June 15, 2006, 18:02:42
Job time : 1907.88 secs

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model1

Run on: June 15, 2006, 17:21:03 ; Search time 62.413 Seconds

(without alignments)
2127.111 Million cell updates/sec

Title: US-09-896-888a-1

Perfect score: 564
Sequence: 1 catgatgatataacatcatgtat.....tgttaccagcacacacatcg 564

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 290227 seqs, 117694381 residues

Total number of hits satisfying chosen parameters: 580454

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications NA New:
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2: /EMC_Celerra_SIDS3/prodata/1/pubpna/US07_NEW_PUB.seq:*
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8: /EMC_Celerra_SIDS3/prodata/1/pubpna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	32.8	5.8	1216	6	US-10-953-349-868 Sequence 868, App
C 2	32.8	5.8	3119	6	US-10-449-902-9093 Sequence 9093, App
C 3	31.6	5.6	1127	6	US-10-449-902-2563 Sequence 2563, App
C 4	31.6	5.6	1128	6	US-10-449-902-19810 Sequence 19810, App
C 5	31.6	5.6	7833	6	US-10-517-441-350 Sequence 350, App
C 6	31.6	5.6	7833	6	US-10-517-441-350 Sequence 624, App
C 7	31.4	5.6	7873	6	US-10-485-397-7 Sequence 7, App1
C 8	31.4	5.6	7943	6	US-10-485-397-8 Sequence 8, App1
C 9	30.8	5.5	1006	6	US-10-449-902-24096 Sequence 24096, App
C 10	30.6	5.4	9353	6	US-10-517-441-462 Sequence 462, App
C 11	30.6	5.4	9353	6	US-10-517-441-736 Sequence 736, App
C 12	30.2	5.4	2019	6	US-10-449-902-22046 Sequence 22046, App
C 13	30.2	5.4	2127	6	US-10-449-902-9697 Sequence 9697, App
C 14	30.0	5.3	1114	6	US-10-953-349-32119 Sequence 32119, App
C 15	30.0	5.3	1237	6	US-10-511-937-430 Sequence 430, App
C 16	30.0	5.3	2214	6	US-10-449-902-25649 Sequence 25649, App
C 17	30.0	5.3	2586	6	US-10-449-902-24650 Sequence 24650, App
C 18	30.0	5.3	2618	6	US-10-449-902-16689 Sequence 16689, App
C 19	30.0	5.3	3107	6	US-10-517-441-401 Sequence 401, App
C 20	29.6	5.2	3501	6	US-10-517-441-499 Sequence 499, App
C 21	29.6	5.2	1266	6	US-10-953-349-1657 Sequence 1657, App
C 22	29.6	5.2	3283	6	US-10-517-441-678 Sequence 678, App
C 23	29.4	5.2	3331	6	US-10-953-349-8124 Sequence 8124, App
C 24	29.2	5.2	2538	7	US-11-217-529-218 Sequence 218, App
C 25	28.4	5.0	838	6	US-10-449-902-9307 Sequence 9307, App

C 26	28.4	5.0	1456	6	US-10-449-902-12236 Sequence 12236, App
C 27	28.4	5.0	2108	6	US-10-953-349-5230 Sequence 5230, App
C 28	28.4	5.0	4611	7	US-11-267-871-717 Sequence 717, App
C 29	28.4	5.0	4644	1	US-09-484-331-19 Sequence 19, App1
C 30	28.4	5.0	5247	1	US-09-484-331-20 Sequence 20, App1
C 31	28.4	5.0	5264	6	US-10-485-397-10 Sequence 10, App1
C 32	28.4	5.0	5314	1	US-09-484-331-27 Sequence 27, App1
C 33	28.4	5.0	5408	6	US-10-485-397-9 Sequence 9, App1
C 34	28.4	5.0	5715	7	US-11-258-392-4 Sequence 4, App1
C 35	28.4	5.0	6233	7	US-11-296-119-10 Sequence 10, App1
C 36	28.4	5.0	9737	1	US-09-484-331-22 Sequence 22, App1
C 37	28.4	5.0	9737	1	US-09-484-331-23 Sequence 23, App1
C 38	28.4	5.0	9737	1	US-09-484-331-28 Sequence 28, App1
C 39	28.4	5.0	9871	1	US-09-484-331-24 Sequence 24, App1
C 40	28.4	5.0	10060	1	US-09-484-331-25 Sequence 25, App1
C 41	28.4	5.0	11772	7	US-11-246-405-17 Sequence 17, App1
C 42	28.2	5.0	1687	7	US-11-242-317-38 Sequence 38, App1
C 43	28.2	5.0	1688	6	US-10-449-902-10918 Sequence 10918, App
C 44	28.2	5.0	2416	7	US-11-289-102-76 Sequence 76, App1
C 45	28.2	5.0	3214	6	US-10-449-902-18041 Sequence 18041, App

ALIGNMENTS

```

RESULT 1
US-10-953-349-868/c
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 868
; LENGTH: 1216
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; US-10-953-349-868

Query Match      5.8%; Score 32.8; DB 6; Length 1216;
Best Local Similarity 53.0%; Pred. No. 0.17;
Matches 70; Conservative 0; Mismatches 62; Indels 0; Gaps 0;

QY 5 ATGATAACAGTATGCTATATGCTTCAACAGCAATCTGTGAACGTGTTT 64
DB 292 AACCCAAACGCGCTTATATCAATCCTCACTACACCTTCCGAAGACTGTCATC 233
QY 65 CATGTTGCCAACAACACCTTATATCTGCGTCCGCCACCAACCACTTTTGCAC 124
DB 232 CATTAAGCTCAATCCGCACTTTGTTGATATCTTACAGTACCAACACTTGATC 173
QY 125 TGCACAAAACA 136
DB 172 GTACAAATACA 161

RESULT 2
US-10-449-902-9093/c
; Sequence 9093, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agricultural Sciences
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USBS THEROP
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902

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; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 9093
; LENGTH: 3119
; TYPE: DNA
; ORGANISM: Oryza sativa
; PUBLICATON INFORMATION:
; DATABASE ACCESSION NUMBER: AK106441
; DATABASE ENTRY DATE: 2002-08-28
; US-10-449-902-9093
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Query Match          5.6%; Score 32.8; DB 6; Length 3119;
Best Local Similarity 67.6%; Pred. No. 0.29;
Matches 46; Conservative 0; Mismatches 22; Indels 0; Gaps 0;
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QY 190 TTTACATTAATGCTACACCGCTGTATGCTTCCCAATACACACACATTTGAACCT 249
    |||||
DB 1385 TTTGAAGAAATGTCACCTCATTTATTCCTCAAAATCCATTGAAAGATTGACCA 1326
    |||||
QY 250 TTTTGCGAG 257
    |||||
DB 1325 TTTTCGAG 1318
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RESULT 3
US-10-449-902-2563/c
; Sequence 2563, Application US/10449902
; Publication No. US20060123505A1
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; GENERAL INFORMATION:
; APPLICANT: National Institute of Agricultural Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; TITLE OF INVENTION: Full-length plant cDNA and uses thereof.
; FILE REFERENCE: MOA-A02051-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 2563
; LENGTH: 1127
; TYPE: DNA
; ORGANISM: Oryza sativa
; PUBLICATON INFORMATION:
; DATABASE ACCESSION NUMBER: AK104298
; DATABASE ENTRY DATE: 2002-08-28
; US-10-449-902-2563
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Query Match          5.6%; Score 31.6; DB 6; Length 1127;
Best Local Similarity 52.2%; Pred. No. 0.43;
Matches 70; Conservative 0; Mismatches 64; Indels 0; Gaps 0;
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QY 347 TGTGTCTTATCGTACAGACGCGCAGCTTCTGTGTGCTAACGCGAGCGGACGAC 406
    |||||
DB 218 TGTGTACTCGCGCTGCGCGCGCGCGCGCTGTCTCCGCAATCGCGGCGCCGAC 159
    |||||
QY 407 TCTTATCGGAACAGACGCGCTTCATATCAGCGCGCTTATCTCATGCGGTGACCG 466
    |||||
DB 158 CTCGACACCAATCTCTCGCGCGCGCGCTCTCCGACGAGATCCAGCGGCGGCTCG 99
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QY 467 GACACGAGGCGCC 480
    |||||
DB 98 GTGACGCTGAGGCC 85
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RESULT 4
US-10-449-902-19810/c
; Sequence 19810, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agricultural Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; TITLE OF INVENTION: Full-length plant cDNA and uses thereof.
; FILE REFERENCE: MOA-A02051-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 19810
; LENGTH: 1128
; TYPE: DNA
; ORGANISM: Oryza sativa
; PUBLICATON INFORMATION:
; DATABASE ACCESSION NUMBER: AK070153
; DATABASE ENTRY DATE: 2001-12-06
; US-10-449-902-19810
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```

Query Match          5.6%; Score 31.6; DB 6; Length 1128;
Best Local Similarity 52.2%; Pred. No. 0.43;
Matches 70; Conservative 0; Mismatches 64; Indels 0; Gaps 0;
```

```

QY 347 TGTGTCTTATCGTACAGACGCGCAGCTTCTGTGTGCTAACCGCGGACCGAC 406
    |||||
DB 219 TGTGTACTCGCGCTGCGCGCGCGCGCTGTCTCCGCAATCGCGGCGCCGAC 160
    |||||
QY 407 TCTTATCGGAACAGACGCGCTTCATATCAGCGCGCTTATCTCATGCGGTGACCG 466
    |||||
DB 159 CTCGACACCAATCTCTCGCGCGCGCGCTCTCCGACGAGATCCGACGCGGCGCTCG 100
    |||||
QY 467 GACACGAGGCGCC 480
    |||||
DB 99 GTGACGCTGAGGCC 86
```

```

RESULT 5
US-10-517-441-350/c
; Sequence 350, Application US/10517441
; Publication No. US20060121467A1
; GENERAL INFORMATION:
; APPLICANT: FOEKEN, John
; APPLICANT: HARBEC, Nadia
; APPLICANT: KOENIG, Thomas
; APPLICANT: MAIER, Sabine
; APPLICANT: MARTENS, John
; APPLICANT: MODEL, Fabian
; APPLICANT: NIMMICH, Inko
; APPLICANT: RUJAN, Tamas
; APPLICANT: SCHMITT, Armin
; APPLICANT: SCHMITT, Manfred
; APPLICANT: LOOK, Maxime P.
; APPLICANT: MARX, Almuth
; APPLICANT: HOEPFLER, Heinz
; TITLE OF INVENTION: Method and nucleic acids for the improved treatment of breast cell
; FILE REFERENCE: 47675-93
; CURRENT APPLICATION NUMBER: US/10/517,441
; CURRENT FILING DATE: 2004-12-11
; PRIOR APPLICATION NUMBER: PCT/EP2003/010861
; PRIOR FILING DATE: 2003-10-01
; PRIOR APPLICATION NUMBER: DE 10317955.0
; PRIOR FILING DATE: 2003-04-17
```

;; PRIOR APPLICATION NUMBER: DE 10300096.8
;; PRIOR FILING DATE: 2003-01-07
;; PRIOR APPLICATION NUMBER: DE 10245779.4
;; PRIOR FILING DATE: 2002-10-01
;; NUMBER OF SEQ ID NOS: 2147
;; SEQ ID NO 350
;; LENGTH: 7833
;; TYPE: DNA
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-517-441-350

Query Match 5.6%; Score 31.6; DB 6; Length 7833;
Best Local Similarity 50.0%; Pred. No. 1.2;
Matches 79; Conservative 0; Mismatches 79; Indels 0; Gaps 0;

Qy 112 AACTTTTGCACGCAAAAAACACGCTTTTGACGCGGCCCATACATGATCAAACT 171
Db 5930 AATATCTTCCATTAATAAAAAAATATTTCTTAATAAAAAAATATATCTACA 5871
Qy 172 CTACGTTTGTAGCTATTTTACATAAATAGCTACACCGTTGTATACGCTCAAAATACA 231
Db 5870 CTATTTCTACTAAAAAATCTAACACTAACTCTACTCTCTACATCATTAATTAATAT 5811
Qy 232 CTACCAACATTTGAACCTTTTTCAGTGCAGCAAAAAAGTA 269
Db 5810 ATATACCAAAATTAATATTTCTAACTCAAAAAAATTA 5773

RESULT 6

US-10-517-441-624/C
; Sequence 624, Application US/10517441
; Publication No. US20060121467A1
; GENERAL INFORMATION:
; APPLICANT: FOEKENS, John
; APPLICANT: HARBECK, Nadia
; APPLICANT: KOENIG, Thomas
; APPLICANT: MAIER, Sabine
; APPLICANT: MARTENS, John
; APPLICANT: MODEL, Fabian
; APPLICANT: NIMMERICH, Inko
; APPLICANT: RUJAN, Tamas
; APPLICANT: SCHMITT, Armin
; APPLICANT: SCHMITT, Manfred
; APPLICANT: LOOK, Maxime P.
; APPLICANT: MARX, Almut
; APPLICANT: HOEFLE, Heinz
; TITLE OF INVENTION: Method and nucleic acids for the improved treatment of breast cell
; FILE REFERENCE: 47675-93
; CURRENT APPLICATION NUMBER: US/10/517,441
; CURRENT FILING DATE: 2004-12-11
; PRIOR APPLICATION NUMBER: PCT/EP2003/010881
; PRIOR FILING DATE: 2003-10-01
; PRIOR APPLICATION NUMBER: DE 10317955.0
; PRIOR FILING DATE: 2003-04-17
; PRIOR APPLICATION NUMBER: DE 10300096.8
; PRIOR FILING DATE: 2003-01-07
; PRIOR APPLICATION NUMBER: DE 10245779.4
; PRIOR FILING DATE: 2002-10-01
; NUMBER OF SEQ ID NOS: 2147
; SEQ ID NO 624
; LENGTH: 7833
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-517-441-624

Query Match 5.6%; Score 31.6; DB 6; Length 7833;
Best Local Similarity 50.0%; Pred. No. 1.2;
Matches 79; Conservative 0; Mismatches 79; Indels 0; Gaps 0;

Qy 112 AACTTTTGCACGCAAAAAACACGCTTTTGACGCGGCCCATACATGATCAAACT 171
Db 5930 AATATCTTCCATTAATAAAAAAATATTTCTTAATAAAAAAATATATCTACA 5871
Qy 172 CTACGTTTGTAGCTATTTTACATAAATAGCTACACCGTTGTATACGCTCAAAATACA 231
Db 5870 CTATTTCTACTAAAAAATCTAACACTAACTCTACTCTCTACATCATTAATTAATAT 5811
Qy 232 CTACCAACATTTGAACCTTTTTCAGTGCAGCAAAAAAGTA 269
Db 5810 ATATACCAAAATTAATATTTCTAACTCAAAAAAATTA 5773

RESULT 7

US-10-485-397-7/C
; Sequence 7, Application US/10485397
; Publication No. US20060099673A1
; GENERAL INFORMATION:
; APPLICANT: ALTRNA Pharma AG
; TITLE OF INVENTION: Novel Recombinant Gene Expression Method
; FILE REFERENCE: B6970SPCT01
; CURRENT APPLICATION NUMBER: US/10/485,397
; CURRENT FILING DATE: 2004-01-30
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7
; LENGTH: 7873
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: pGFPetopneo is a circular Plasmid DNA
US-10-485-397-7

Query Match 5.6%; Score 31.4; DB 6; Length 7873;
Best Local Similarity 45.9%; Pred. No. 1.5;
Matches 107; Conservative 0; Mismatches 126; Indels 0; Gaps 0;

Qy 321 CGAATCATTATTCGACCGGAGAGTGTGTTTATCTGTACAGACCGCACTTCTCG 380
Db 4319 CCAACCAAGATAGCCGCGCTCGCTTGTGACATTCATTCAGGGACCGGACAGGTCGG 4260
Qy 381 TGTGTGTAACCGAGCGGAGCGCACTCTTATCGAACAAGAGCGGCTTCATTCAGC 440
Db 4259 TCTTGACAAAGAAAGACCGGCGCCCTGCGCTGACAGCGGAAACAGCGGCAATCAGAGC 4200
Qy 441 CGCGCGTTATCTCATCGCGCTGACCGGACAGAGCGCGCCGCTTATCGCGCTTAT 500
Db 4199 AGCCGATGTCTTGTGCGCCCACTCATAGCCGAATAGCCTCTCACCAGCGGCGGAG 4140
Qy 501 AAATACGCGCGCAAGATCTGTTAAACACAGTTGAACAGCATCTGTACAGC 553
Db 4139 AACCTCGTGCAATCATCTTGTTCATATCTAGTTCAACTAGACTGTGTACAGC 4087

RESULT 8

US-10-485-397-8/C
; Sequence 8, Application US/10485397
; Publication No. US20060099673A1
; GENERAL INFORMATION:
; APPLICANT: ALTRNA Pharma AG
; TITLE OF INVENTION: Novel Recombinant Gene Expression Method
; FILE REFERENCE: B6970SPCT01
; CURRENT APPLICATION NUMBER: US/10/485,397
; CURRENT FILING DATE: 2004-01-30
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8
; LENGTH: 7943
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: pGFPetopneoSecs is a circular Plasmid DNA

Query Match 5.6%; Score 31.6; DB 6; Length 7943;
Best Local Similarity 50.0%; Pred. No. 1.2;
Matches 79; Conservative 0; Mismatches 79; Indels 0; Gaps 0;

US-10-485-397-8

Query Match 5.6%; Score 31.4; DB 6; Length 7943;
Best Local Similarity 45.9%; Pred. No. 1.5;
Matches 107; Conservative 0; Mismatches 126; Indels 0; Gaps 0;

Qy 321 CGATCATATTATGAGACCGGAGAGTGTCTTATCGAGACGAGCCAGCTTCTG 380
Db 4319 CCAAGCCAGATAGCGGGGCTGCTCGCTTGTGCAATTATTCAGGACCGGACAGGTGCG 4260
Qy 381 TGTGTACCGGACCGGAGCGCAACTCTTATCGGAACGAGCGCTTCATATCAGC 440
Db 4259 TCTTGAACAAAAGAACCGGGGGCCCTCGCGCTGACAGCCGGAACAGCGCGCATCAAGC 4200
Qy 441 CGGCGCTTATCTATGCGCGTGAACCGGACGAGCGCCGCTCCGCTTATCGCGCTAT 500
Db 4199 AGCCGATGTCTGTGTGGCCAGTCATAGCCGAATACCTCTCCACCCAGCGCGGAG 4140
Qy 501 AATATACAGCCGCAACGATGTGTAAACAGTGAACAGCATCTGTACAGC 553
Db 4139 AACTGCGTGAATCCATCTTTCATATCTAGTTCACTAGTTCTTGTACAGC 4087

RESULT 9

US-10-449-902-24096/c
Sequence 24096, Application US/10449902
Publication No. US20060123505A1

GENERAL INFORMATION:
APPLICANT: National Institute of Agricultural Sciences.
APPLICANT: Bio-oriented Technology Research Advancement Institution.
APPLICANT: The Institute of Physical and Chemical Research.
APPLICANT: Foundation for Advancement of International Science.
TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
FILE REFERENCE: MOA-A02051-US
CURRENT APPLICATION NUMBER: US/10/449, 902
CURRENT FILING DATE: 2003-05-29
PRIOR APPLICATION NUMBER: JP 2002-203269
PRIOR FILING DATE: 2002-05-30
PRIOR APPLICATION NUMBER: JP 2002-383870
PRIOR FILING DATE: 2002-12-11
NUMBER OF SEQ ID NOS: 56791
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 24096
LENGTH: 1006
TYPE: DNA
ORGANISM: Oryza sativa
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: AK099538
DATABASE ENTRY DATE: 2002-08-28
US-10-449-902-24096

Query Match 5.5%; Score 30.8; DB 6; Length 1006;
Best Local Similarity 51.4%; Pred. No. 0.77;
Matches 71; Conservative 0; Mismatches 67; Indels 0; Gaps 0;

Qy 160 ATAGTACAACTCTAGCTTGTAGACTATTTTACATTAATAGCTACACCGTGTATAC 219
Db 898 AGATGACAACTCTAGCTTGTAGAGAAAAAAGACATCTAGCTGTTAACTAA 839
Qy 220 GCTTCAAAATACACTACACACATTTGAGAGTCAAAAAAGTACGTGTGCGCA 279
Db 838 GGTGCTACTACTATGATGATGAGACAAATTAACAAGAAATGCTTAATGTTGATGCG 779
Qy 280 GTACAGTACGCGCGCTT 297
Db 778 TGCTGATGTGCTGCTT 761

RESULT 10

US-10-517-441-462/c
Sequence 462, Application US/10517441
Publication No. US20060121467A1
GENERAL INFORMATION:

APPLICANT: FOEKENS, John
APPLICANT: HARBECK, Nadia
APPLICANT: KOENIG, Thomas
APPLICANT: MAIER, Sabine
APPLICANT: MARTENS, John
APPLICANT: MODEL, Fabian
APPLICANT: NIMMERICH, Inko
APPLICANT: RUJAN, Tamas
APPLICANT: SCHMITT, Armin
APPLICANT: SCHMITT, Manfred
APPLICANT: LÖCK, Maxime P.
APPLICANT: MARX, Almut
APPLICANT: HOEFLER, Heinz
TITLE OF INVENTION: Method and nucleic acids for the improved treatment of breast cell
FILE REFERENCE: 47675-93
CURRENT APPLICATION NUMBER: US/10/517,441
CURRENT FILING DATE: 2004-12-11
PRIOR APPLICATION NUMBER: PCT/EP2003/010881
PRIOR FILING DATE: 2003-10-01
PRIOR APPLICATION NUMBER: DE 10317955.0
PRIOR FILING DATE: 2003-04-17
PRIOR APPLICATION NUMBER: DE 10300096.8
PRIOR FILING DATE: 2003-01-07
PRIOR APPLICATION NUMBER: DE 10245779.4
PRIOR FILING DATE: 2002-10-01
NUMBER OF SEQ ID NOS: 2147
SEQ ID NO 462
LENGTH: 9353
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Chemically treated genomic DNA (Homo sapiens)
US-10-517-441-462

Query Match 5.4%; Score 30.6; DB 6; Length 9353;
Best Local Similarity 49.1%; Pred. No. 3;
Matches 81; Conservative 0; Mismatches 84; Indels 0; Gaps 0;

Qy 10 AATCATGTATGTGCTATGTTGCTTCAACAACATTTCTGTGAACGTGTTTCAATGT 69
Db 8082 ATAAATTTATCTTACTAATTTCTAAATTAACAACCTTATCTTCAATTTCTTAAAT 8023
Qy 70 TTGCAACAAGACCTTTATCTCGGTGCGCTCCGACCAACCTTTTTCAGTGCAC 129
Db 8022 TCTAAATCAACCCATCAAACTTTCTAACCTTAAACATCAAAAAATCTACTTTTA 7963
Qy 130 AAAACACGCTTTTGACGCGGCGCCATACATAGTACAACTCTA 174
Db 7962 ATAAAAACTTACTTAACCAACACTTAATATACAAACAACTA 7918

RESULT 11

US-10-517-441-736/c
Sequence 736, Application US/10517441
Publication No. US20060121467A1

GENERAL INFORMATION:
APPLICANT: FOEKENS, John
APPLICANT: HARBECK, Nadia
APPLICANT: KOENIG, Thomas
APPLICANT: MAIER, Sabine
APPLICANT: MARTENS, John
APPLICANT: MODEL, Fabian
APPLICANT: NIMMERICH, Inko
APPLICANT: RUJAN, Tamas
APPLICANT: SCHMITT, Armin
APPLICANT: SCHMITT, Manfred
APPLICANT: LÖCK, Maxime P.
APPLICANT: MARX, Almut
APPLICANT: HOEFLER, Heinz
TITLE OF INVENTION: Method and nucleic acids for the improved treatment of breast cell
FILE REFERENCE: 47675-93

CURRENT APPLICATION NUMBER: US/10/517,441
CURRENT FILING DATE: 2004-12-11
PRIORITY APPLICATION NUMBER: PCT/EP2003/010881
PRIORITY FILING DATE: 2003-10-01
PRIORITY APPLICATION NUMBER: DE 10317955.0
PRIORITY FILING DATE: 2003-04-17
PRIORITY APPLICATION NUMBER: DE 10300096.8
PRIORITY FILING DATE: 2003-01-07
PRIORITY APPLICATION NUMBER: DE 10245779.4
PRIORITY FILING DATE: 2002-10-01
NUMBER OF SEQ ID NOS: 2147
SEQ ID NO 736
LENGTH: 9353
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-517-441-736

Query Match 5.4%; Score 30.6; DB 6; Length 9353;
Best Local Similarity 49.1%; Pred. No. 3;
Matches 81; Conservative 0; Mismatches 84; Indels 0; Gaps 0;

QY 10 AACAAATGATGGTATGCTTATGCTTCAACAACATTTGTTGAAGTGTTCATGT 69
DB 8082 ATAAATTTTCTTACTTAATTAATTAACACCTTACTTTCAAAATTTCTTAAAT 8023
QY 70 TTGCCAACAAGACCTTTATCTGCTGCGCTCCCAACAACCTTTTGGACGTGCA 129
DB 8022 TCTAAATCAAAACCATCAAAACCTTTTACCTCAAAAACATCAAAAATCTAATTT 7963
QY 130 AAAAACAAGCTTTTGCACGGGGCCCATACATAGTACAACTCTA 174
DB 7962 ATAAAAACTTACTTAACCAACACTATATACAAACACACTA 7918

RESULT 12

US-10-449-902-22046
Sequence 22046, Application US/10449902
Publication No. US20060123505A1
GENERAL INFORMATION:
APPLICANT: National Institute of Agricultural Sciences.
APPLICANT: Bio-oriented Technology Research Advancement Institution.
APPLICANT: The Institute of Physical and Chemical Research.
APPLICANT: Foundation for Advancement of International Science.
TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
FILE REFERENCE: MOA-A0205Y1-US
CURRENT APPLICATION NUMBER: US/10/449,902
PRIORITY FILING DATE: 2003-05-29
PRIORITY APPLICATION NUMBER: JP 2002-203269
PRIORITY FILING DATE: 2002-05-30
PRIORITY APPLICATION NUMBER: JP 2002-383870
PRIORITY FILING DATE: 2002-12-11
NUMBER OF SEQ ID NOS: 56791
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 22046
LENGTH: 2019
TYPE: DNA
ORGANISM: Oryza sativa
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: AK072256
DATABASE ENTRY DATE: 2001-12-06
US-10-449-902-22046

Query Match 5.4%; Score 30.2; DB 6; Length 2019;
Best Local Similarity 55.1%; Pred. No. 1.8;
Matches 59; Conservative 0; Mismatches 48; Indels 0; Gaps 0;

QY 388 AACCGACGCGGACGCACTCTTATGGAACAGAGCGCCCTCCATATACGCGCGGT 447
DB 1562 AACGTCATCAGAGCGCGCTCCCTCCCGACGCGCGCGCCAGCGCGCTGCGCGT 1621
QY 448 TATCTATGCGGTGACCGGACAGAGCGCGCGCTCCGCTTATCGC 494

DB 1622 GACCTATCCGCGCGCTCTGCTAAGAGCCCAAGCGGATCCG 1668

RESULT 13

US-10-449-902-9697
Sequence 9697, Application US/10449902
Publication No. US20060123505A1
GENERAL INFORMATION:
APPLICANT: National Institute of Agricultural Sciences.
APPLICANT: Bio-oriented Technology Research Advancement Institution.
APPLICANT: The Institute of Physical and Chemical Research.
APPLICANT: Foundation for Advancement of International Science.
TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
FILE REFERENCE: MOA-A0205Y1-US
CURRENT APPLICATION NUMBER: US/10/449,902
PRIORITY FILING DATE: 2003-05-29
PRIORITY APPLICATION NUMBER: JP 2002-203269
PRIORITY FILING DATE: 2002-05-30
PRIORITY APPLICATION NUMBER: JP 2002-383870
PRIORITY FILING DATE: 2002-12-11
NUMBER OF SEQ ID NOS: 56791
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 9697
LENGTH: 2127
TYPE: DNA
ORGANISM: Oryza sativa
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: AK107045
DATABASE ENTRY DATE: 2002-08-28
US-10-449-902-9697

Query Match 5.4%; Score 30.2; DB 6; Length 2127;
Best Local Similarity 55.1%; Pred. No. 1.9;
Matches 59; Conservative 0; Mismatches 48; Indels 0; Gaps 0;

QY 388 AACCGACGCGGACGCACTCTTATGGAACAGAGCGCCCTCCATATACGCGCGGT 447
DB 1543 AACGTCATCAGAGCGCGCTCCCTCCCGACGCGCGCGCCAGCGCGCTGCGCGT 1602
QY 448 TATCTATGCGGTGACCGGACAGAGCGCGCGCTCCGCTTATCGC 494
DB 1603 GACCTATCCGCGCGCTCTGCTAAGAGCCCAAGCGGATCCG 1649

RESULT 14

US-10-953-349-32119/c
Sequence 32119, Application US/10953349
Publication No. US20060107345A1
GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nikolai et al.
APPLICANT: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCODED THERBY
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
PRIORITY FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PatentIn version 3.3
SEQ ID NO 32119
LENGTH: 1114
TYPE: DNA
ORGANISM: Triticum aestivum
US-10-953-349-32119

Query Match 5.3%; Score 30; DB 6; Length 1114;
Best Local Similarity 53.4%; Pred. No. 1.5;
Matches 63; Conservative 0; Mismatches 55; Indels 0; Gaps 0;

QY 379 TGTGTGCTAACGACGCGGACGCACTCTTATGGAACAGAGCGCGCTCCATATCA 438
DB 955 TGTGTGCGATGACAGACAGACGAGACAGACAGCTGTCAAAAGCGCGCGGAGCGGC 896
QY 439 GCGCGCGCTTATCTATGCGCGGTGACCGGACAGAGCGCGCGCTCCGCTTATCGGC 496

Db 895 GCCGATGCGTTCGTCGCGGGCTCGACGGGGCGGCTGGCTCCGCGC 838

```

RESULT 15
US-10-511-937-430/c
; Sequence 430. Application US/10511937
; Publication No. US20060088836A1
; GENERAL INFORMATION:
; APPLICANT: EXPRESSION DIAGNOSTICS, INC.
; APPLICANT: Wohlgenuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; APPLICANT: Prentice, James
; APPLICANT: Morris, MacDonald
; APPLICANT: Rosenberg, Steven
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
; TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION
; FILE REFERENCE: 506612000104
; CURRENT APPLICATION NUMBER: US/10/511,937
; CURRENT FILING DATE: 2004-10-19
; PRIOR APPLICATION NUMBER: PCT/US2003/012946
; PRIOR FILING DATE: 2003-04-24
; PRIOR APPLICATION NUMBER: US 10/131,831
; PRIOR FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 10/325,899
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 3117
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 430
; LENGTH: 1237
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-511-937-430

```

Query Match	5.3%	Score 30	DB 6	Length 1237
Best Local Similarity	67.7%	Pred. No. 1.6		
Matches 42; Conservative	0	Mismatches 20	Indels 0	Gaps 0

Qy	26	TATGTTGCTTCAACAACAATTCTGTTGA	CTGCTTTCATGTTGCCAACAGCACC	85
Db	1228	TATGTTGCATTGAGAACTTTATATGTA <td>AGCCGATTTTTCATGTTGCCAGTAGCCTCT</td> <td>11659</td>	AGCCGATTTTTCATGTTGCCAGTAGCCTCT	11659

QY	86	TT	87
Db	1168	GT	1167

Search completed: June 15, 2006, 18:04:16
Job time : 64.413 secs

GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: June 15, 2006, 16:18:24 ; Search time 189.421 Seconds
(without alignments)
6515.052 Million cell updates/sec

Title: US-09-896-888a-1_COPY_351_527

Perfect score: 177

Sequence: 1 gcttatacgcagacgacgc.....gccccaacgactctgtraa 177

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 10489840

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : N_Geneseq_8:*

- 1: geneseqn1980s:*
- 2: geneseqn1990s:*
- 3: geneseqn2000s:*
- 4: geneseqn2001as:*
- 5: geneseqn2001bs:*
- 6: geneseqn2002as:*
- 7: geneseqn2002bs:*
- 8: geneseqn2003as:*
- 9: geneseqn2003bs:*
- 10: geneseqn2003cs:*
- 11: geneseqn2003ds:*
- 12: geneseqn2004as:*
- 13: geneseqn2004bs:*
- 14: geneseqn2005s:*
- 15: geneseqn2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	177	100.0	560	12	ADQ48575
2	177	100.0	564	2	AAV62487
3	177	100.0	2773	9	AAI61306
4	175.4	99.1	5038	12	ADQ48539
5	41	23.2	141	12	ADQ48576
6	32	18.1	921	3	AAA02474
7	31	17.5	2109	14	ADY37449
8	30.8	17.4	1268	4	ABL18801
9	30.8	17.4	1342	4	ABL27503
10	30.8	17.4	3408	4	ABL27502
11	30.8	17.4	3600	4	ABL18800
12	30.6	17.3	29169	10	ADT47065
13	30.6	17.3	1404	13	ADT47065
14	30.6	17.3	10968	14	AECT5808
15	30.6	17.3	78869	14	AECT5808
16	30.2	17.1	1127	14	AEET5774
17	30	16.9	657	12	AD145632
18	30	16.9	1710	11	ABD14088

C	19	30	16.9	2485	15	AEP55630	Aef55630 Human gen
C	20	30	16.9	3107	13	ADS89385	Ad89385 Oligonucle
C	21	30	16.9	3501	13	ADS89483	Ad89483 Oligonucle
C	22	30	16.9	6107	6	ABK31430	Abk31430 Signal tr
C	23	30	16.9	6107	6	ABL70389	Ab170389 Chemical
C	24	30	16.9	6107	6	AA61341	AA61341 Human gen
C	25	30	16.9	132544	13	ADY99887	Ady99887 Nanchangm
C	26	29.8	16.8	1311	14	ACI65908	Ac165908 M. xanthu
C	27	29.8	16.8	1370	6	ADP83430	Adp83430 Bread whe
C	28	29.8	16.8	1789	4	ABL19245	Ab119245 Drosophi
C	29	29.8	16.8	3915	4	ABL19244	Ab119244 Drosophi
C	30	29.8	16.8	13579	14	ACI64638	Ac164638 M. xanthu
C	31	29.6	16.7	300	3	AAA01209	AAa01209 Human col
C	32	29.6	16.7	1798	13	ADT18768	Adt18768 Plant cDN
C	33	29.2	16.5	1593	13	ADT45665	Adt45665 Bacteri
C	34	28.6	16.2	585	11	ABD13766	Abd13766 Pseudom
C	35	28.6	16.2	823	12	ACH89781	ACH89781 Human gen
C	36	28.6	16.2	915	5	AA870780	AA870780 Human gen
C	37	28.6	16.2	1425	4	AA851490	AA851490 Pseudom
C	38	28.6	16.2	1425	8	ACA19456	ACA19456 Prokaryot
C	39	28.6	16.2	1434	13	ADS56860	Ad56860 Bacteri
C	40	28.6	16.2	1443	11	ABD13493	Abd13493 Pseudom
C	41	28.6	16.2	1551	11	ABD13719	Abd13719 Pseudom
C	42	28.6	16.2	2085	11	ABD13633	Abd13633 Pseudom
C	43	28.6	16.2	2088	15	AER86025	Aer86025 Human neu
C	44	28.6	16.2	2091	2	AA806989	AA806989 Human neu
C	45	28.6	16.2	2091	6	ABK90730	ABK90730 CDNA enco

ALIGNMENTS

RESULT 1	ADQ48575	standard; DNA; 560 BP.
ID	ADQ48575	
XX	ADQ48575	
AC	ADQ48575	
DT	09-SEP-2004	(first entry)
XX		
DE	OpIE2 promoter DNA sequence.	
XX		
KM	viral vector; recombination site; recombinant virus;	
KW	replication-defective particle generation; gene expression inhibition;	
KM	gene therapy vector; ds; OpIE2 promoter.	
XX		
OS	Unidentified.	
PN	W02004009768-A2.	
XX		
PD	29-JAN-2004.	
XX		
PF	18-JUL-2003; 2003WO-US022437.	
XX		
PR	18-JUL-2002; 2002US-0396335P.	
PR	26-JUL-2002; 2002US-0398617P.	
PR	19-NOV-2002; 2002US-0427231P.	
PR	24-MAR-2003; 2003US-0456496P.	
XX	03-JUN-2003; 2003US-0474940P.	
PA	(INV-) INVTROGEN CORP.	
PA	(BENN) BENNETT R P.	
PA	(WELC) WELCH P J.	
PA	(HARW) HARWOOD S.	
PA	(MADD) MADDEN K.	
PA	(FRIM) FRIMPONG K.	
PA	(FRAN) FRANKS K E.	
XX		
PI	Bennett RP, Welch PJ, Harwood S, Madden K, Frimping K, Franke KE;	
XX		
DR	WPI; 2004-132944/13.	
XX		
PT	Novel nucleic acid molecule comprising all or a portion of one or more	

PT viral genome and further comprising two or more recombination sites that
 PT do not substantially recombine with each other, useful as gene therapy.
 XX
 XS Disclosure; Fig 16; 55pp; English.

The invention comprises a nucleic acid molecule consisting of all or a portion of one or more viral/baculoviral genomes and further containing at least two recombination sites that do not substantially recombine with each other. One or more of the recombination sites is capable of undergoing recombination with a compatible recombination site in the presence of one or more proteins active in lambda recombination. The nucleic acid of the invention replicates in prokaryotic and eukaryotic cells. The nucleic acid of the invention is useful for constructing a recombinant virus, generating replication-defective particles, preventing/inhibiting the expression of one or more genes in an organism, and are useful as gene therapy vectors. The nucleic acid of the invention is also useful for producing and expressing fusion polypeptides. The present DNA sequence represents the OpIE2 promoter that was used in the exemplification of the invention.

SQ Sequence 560 BP; 144 A; 156 C; 116 G; 144 T; 0 U; 0 Other;

Query Match	100.0%	Score 177;	DB 12;	Length 560;
Best Local Similarity	100.0%	Pred. No. 3.1e-48;		
Matches 177; Conservative	0;	Mismatches	0;	Gaps 0;

Qy	Db
1	355
GTCTTATCGTCAGACAGCGCCAGCTTCTGTGTGTTGCTAACCGCAGCCGGACGCACACTTCT	GTCTTATCGTCAGACAGCGCCAGCTTCTGTGTGTTGCTAACCGCAGCCGGACGCACACTTCT
60	414

QY	61	TATCGAACACGAGACGGCCCTTCATATACGCGCGCGCTTATCTCATGCGCGGTACCGGACA	120
Db	415	TATCGAACACGAGACGGCCCTTCATATACGCGCGCGCTTATCTCATGCGCGGTACCGGACA	474

Oy 121 CGAGGCGCCCGTCCCGCTATCGCGCTATAAATACAGCCGCACGATCTGTAA 177
|||||
|||
D6 475 CGAGGCGCCCGTCCCGCTATCGCGCTATAAATACAGCCGCACGATCTGTAA 531

RESULT 2
AAV62487
ID AAV62487 standard; DNA; 564 BP.

XX	17-OCT-2003	(revised)
DT	19-JAN-1999	(first entry)
DT		

O. pseudotsugata multicapsid nucleopolyhedrosis virus 122 promoter.

KM *Oryzias pseudotetrastus*; multicapsid; nucleopolydnavirus; OpNPV,
KM *Op1*, promoter; shuttle vector; transformation; melanotransferrin,
KM immediate early baculovirus promoter; prokaryotic; transciption,
KM bleomycin/plaemycin-type antitibiotic; insect cell; transposon,
KM ion transport peptide hormone; ss.

OS *Orgyia pseudotsugata*; polyhedrosis virus.

PN WO9844141-A2.

PD 08-OCT-1998.

PF 26-MAR-1998; 98WO-CA000282.

PR 27-MAR-1997; 97US-0049946P.

XX

XX

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100	101	102	103	104	105	106	107	108	109	110	111	112	113	114	115	116	117	118	119	120	121	122	123	124	125	126	127	128	129	130	131	132	133	134	135	136	137	138	139	140	141	142	143	144	145	146	147	148	149	150	151	152	153	154	155	156	157	158	159	160	161	162	163	164	165	166	167	168	169	170	171	172	173	174	175	176	177	178	179	180	181	182	183	184	185	186	187	188	189	190	191	192	193	194	195	196	197	198	199	200	201	202	203	204	205	206	207	208	209	210	211	212	213	214	215	216	217	218	219	220	221	222	223	224	225	226	227	228	229	230	231	232	233	234	235	236	237	238	239	240	241	242	243	244	245	246	247	248	249	250	251	252	253	254	255	256	257	258	259	260	261	262	263	264	265	266	267	268	269	270	271	272	273	274	275	276	277	278	279	280	281	282	283	284	285	286	287	288	289	290	291	292	293	294	295	296	297	298	299	300	301	302	303	304	305	306	307	308	309	310	311	312	313	314	315	316	317	318	319	320	321	322	323	324	325	326	327	328	329	330	331	332	333	334	335	336	337	338	339	340	341	342	343	344	345	346	347	348	349	350	351	352	353	354	355	356	357	358	359	360	361	362	363	364	365	366	367	368	369	370	371	372	373	374	375	376	377	378	379	380	381	382	383	384	385	386	387	388	389	390	391	392	393	394	395	396	397	398	399	400	401	402	403	404	405	406	407	408	409	410	411	412	413	414	415	416	417	418	419	420	421	422	423	424	425	426	427	428	429	430	431	432	433	434	435	436	437	438	439	440	441	442	443	444	445	446	447	448	449	450	451	452	453	454	455	456	457	458	459	460	461	462	463	464	465	466	467	468	469	470	471	472	473	474	475	476	477	478	479	480	481	482	483	484	485	486	487	488	489	490	491	492	493	494	495	496	497	498	499	500	501	502	503	504	505	506	507	508	509	510	511	512	513	514	515	516	517	518	519	520	521	522	523	52
--	---	---	---	---	---	---	---	---	---	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	----

[illegible]

PT Expression vectors for transforming insect cells from disparate lines -
PT useful to express heterologous DNA, e.g. to allow study of gene
PT expression and produce commercially important proteins.
XX
PS Claim 10; Page 82; 121pp; English.

This represents a *Oryza pseudotirugata* multicapsid nucleopolyhedrovirus (OpMNPV) immediate early 2 (Op Ie2) promoter sequence. The invention provides a new shuttle vector for transforming insect cells that comprises: (i) prokaryotic origin of replication; (ii) insect promoter having homology to, and capable of functioning as, an immediate early baculovirus promoter; (iii) prokaryotic promoter sequence, and (iv) selectable marker capable of conferring resistance to a bleomycin/ phleomycin-type antibiotic under transcriptional control of (ii) and (iii), in insect and prokaryotic cells respectively. The vectors can be used to stably transform (especially insect) cells with heterologous DNA, useful to allow study of gene expression and direct expression of heterologous gene products e.g. commercially important proteins. They are especially useful to allow expression of the heterologous melanotransferrins, ion transport peptide hormones or biologically active derivatives in insect cells. They enable transformation of insect cell lines from disparate species, allowing screening of lines for optimum post-translational modification of particular proteins. Shuttle vectors further comprising DNA transposable elements defining a transposon can be used to optimise heterologous protein expression and facilitate selection of desired transformants. (Updated on 17-Oct-2003 to standardise OS field)

Sequence 564 BP; 147 A; 160 C; 116 G; 141 T; 0 U; 0 Other;

Query Match	100.0%	Score 177;	DB 2;	Length 564;
Best Local Similarity	100.0%;	Pred. No. 3.1e-48;		
Matches 177; Conservative	0;	Mismatches	0;	Gaps 0;

```
QY      1 GTCTTATCGTGACAGGACGCCAGTTTCGTGTGGTAACCCGACGCCAATTCTT    60
        |||
Db     351 GTCTTATCGTGACAGGACGCCAGTTTCGTGTGGTAACCCGACGCCAATTCTT    411
```

QY 61 TATCGGAACAGAGCGCGCTCCATTCACGCGCGCTTATCTCATGGCGGTGACCGGACA 120
|||||
Db 411 TATCGGAACAGAGCGCGCTCCATTCACGCGCGCTTATCTCATGGCGGTGACCGGACA 470

QY 121 CGAGGCGCCGTCGCCGTTATCGCGCTATAATACAGCCCCGCAACGATCTGTAA 177

D8 471 CGAGGCGCCGTCGCCGTTATCGCGCTATAATACAGCCCCGCAACGATCTGTAA 527

RESULT 3
AAL61306
ID AAL61306 standard; DNA; 2773 BP.

AC AAL61306;

DT 22-SEP-2003 (first entry)

DE p220p2f expression vector for insect cells.

KW Multimeric protein; interleukin 5; IL5; TNFalpha; inflammatory disease;

XX

XX

XX

XX

XX

PR 16-NOV-2001; 2001US-0331575P.

PA (PHAR-) PHARMEXA AS.
PA (KLYS/) KLYSNER S.

PA (NIEL/) NIELSEN F. S.
PA (BRAT/) BRATT T.
PA (VOLD/) VOLDORGB. B.
PA (MOUR/) MOURITSEN S.
PI Klynsner S, Nielsen FS, Bratt T, Voldborg B, Mouritsen S;
XX WPI; 2003-449558/42.
XX
PT New immunogenic analogue of a polymeric protein, useful for preparing a
XX composition for treating inflammatory diseases e.g. arthritis.
XX
PS Disclosure; Page 195-196; 196pp; English.
XX
CC The invention relates to immunogenic analogues of multimeric proteins
CC such as immunogenic variants of interleukin 5 (IL5) and tumour necrosis
CC factor alpha (TNF, TNFalpha) and methods for production of immunogenic
CC analogues. The immunogenic analogue is useful for preparing a composition
CC for treating inflammatory diseases, e.g., arthritis. It is also used in
CC gene therapy. The present sequence is p2ZOP2F expression vector for
CC insect cells. This sequence is used to illustrate the method of the
CC invention
XX
SQ Sequence 2773 BP; 669 A; 750 C; 673 G; 681 T; 0 U; 0 Other;
XX
Query Match 100.0%; Score 177; DB 9; Length 2773;
Best Local Similarity 100.0%; Pred. No. 4.5e-48;
Matches 177; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GCTTATCGTGACGAGCGCAGCTTCTGTGTGCTAACCGCAGCGCAACTCCT 60
DB 355 GTCTTATCGTGACGAGCGCAGCTTCTGTGTGCTAACCGCAGCGCAACTCCT 414
QY 61 TATCGGAACGAGCGCGCTTCATATCAGCCGCGGTTATTCATGCGCGTACCGGACA 120
DB 415 TATCGGAACGAGCGCGCTTCATATCAGCCGCGGTTATTCATGCGCGTACCGGACA 474
QY 121 CGAGGCGCCCGTCCGCTTATCGCGCCTATAATACGCCCGCAACGATCTGTTAA 177
DB 475 CGAGGCGCCCGTCCGCTTATCGCGCCTATAATACGCCCGCAACGATCTGTTAA 531
RESULT 4
ADQ48539
ID ADQ48539 standard; DNA; 5038 BP.
XX
AC ADQ48539;
XX
DT 09-SEP-2004 (first entry)
XX
DE Viral vector-related plasmid - PIB/V5-His-DEST.
XX
KW viral vector; recombination site; recombinant virus;
KW replication-defective particle generation; gene expression inhibition;
KW gene therapy vector; ds; plasmid.
XX
OS Unidentified.
XX
XX WO2004009768-A2.
XX
PD 29-JAN-2004.
XX
PF 18-JUL-2003; 2003WO-US022437.
XX
XX 18-JUL-2002; 2002US-0396335P.
XX 26-JUL-2002; 2002US-0398617P.
XX 19-NOV-2002; 2002US-0427231P.
XX 24-MAR-2003; 2003US-0456496P.
XX 03-JUN-2003; 2003US-0474940P.
XX
XX (INVT-) INVITROGEN CORP.
XX (BENN/) BENNETT R P.
XX (WELC/) WELCH P J.

PA (HARW/) HARWOOD S.
PA (MADD/) MADDEN K.
PA (FRIM/) FRIMPONG K.
PA (FRAN/) FRANK K E.
PI Bennett RP, Welch PJ, Harwood S, Madden K, Frimpong K, Franke KE;
XX WPI; 2004-132944/13.
XX
XX
XX Novel nucleic acid molecule comprising all or a portion of one or more
PT viral genome and further comprising two or more recombination sites that
PT do not substantially recombine with each other, useful as gene therapy.
XX
XX
PS Example 18; Page 395-403; 555pp; English.
XX
CC The invention comprises a nucleic acid molecule consisting of all or a
CC portion of one or more viral/baculoviral genomes and further containing
CC at least two recombination sites that do not substantially recombine with
CC each other. One or more of the recombination sites is capable of
CC undergoing recombination with a compatible recombination site in the
CC presence of one or more proteins active in lambda recombination. The
CC nucleic acid of the invention replicates in prokaryotic and eukaryotic
CC cells. The nucleic acid of the invention is useful for constructing a
CC recombinant virus, generating replication-defective particles,
CC preventing/inhibiting the expression of one or more genes in an organism,
CC and are useful as gene therapy vectors. The nucleic acid of the invention
CC is also useful for producing and expressing fusion polypeptides. The
CC present DNA sequence represents a plasmid that was used in the
CC exemplification of the invention.
XX
SQ Sequence 5038 BP; 1342 A; 1178 C; 1198 G; 1320 T; 0 U; 0 Other;
XX
Query Match 99.1%; Score 175.4; DB 12; Length 5038;
Best Local Similarity 99.4%; Pred. No. 1.8e-47;
Matches 176; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GCTTATCGTGACGAGCGCAGCTTCTGTGTGCTAACCGCAGCGCAACTCCT 60
DB 351 GTCTTATCGTGACGAGCGCAGCTTCTGTGTGCTAACCGCAGCGCAACTCCT 410
QY 61 TATCGGAACGAGCGCGCTTCATATCAGCCGCGGTTATTCATGCGCGTACCGGACA 120
DB 411 TATCGGAACGAGCGCGCTTCATATCAGCCGCGGTTATTCATGCGCGTACCGGACA 470
QY 121 CGAGGCGCCCGTCCGCTTATCGCGCCTATAATACGCCCGCAACGATCTGTTAA 177
DB 471 CGAGGCGCCCGTCCGCTTATCGCGCCTATAATACGCCCGCAACGATCTGTTAA 527
RESULT 5
ADQ48576
ID ADQ48576 standard; DNA; 141 BP.
XX
AC ADQ48576;
XX
DT 09-SEP-2004 (first entry)
XX
DE Viral vector-related plasmid PIB/V5-His-DEST recombination region #1.
XX
KW viral vector; recombination site; recombinant virus;
KW replication-defective particle generation; gene expression inhibition;
KW gene therapy vector; ds; plasmid; recombination region.
XX
OS Unidentified.
XX
XX WO2004009768-A2.
XX
PD 29-JAN-2004.
XX
PF 18-JUL-2003; 2003WO-US022437.
XX
XX 18-JUL-2002; 2002US-0396335P.
XX 26-JUL-2002; 2002US-0398617P.

PT New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signaling and cell-cell
PT interactions.
XX
PS Claim 1; SEQ ID NO 33982; 21pp + Sequence Listing; English.
XX
CC The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signaling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (AB16176-AB130511), expressed DNA
CC sequences (AB101840-AB16175) and the encoded proteins (AB57737-
CC AB572072). The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 1342 BP; 324 A; 347 C; 372 G; 299 T; 0 U; 0 Other;
Query Match 17.4%; Score 30.8; DB 4; Length 1342;
Best Local Similarity 55.7%; Pred. No. 6.7;
Matches 59; Conservative 0; Mismatches 47; Indels 0; Gaps 0;
QY 17 ACCGCCAGCTTCCTGTGTTGCTAACCGGAGCCGAGCGAACTCTTATCGGAACAGACGC 76
DB 731 ACAACAGCTTCCTGTGAGGTGCGCCACAGCGGGTCTTATGCGGCTCCGGTGC 790
QY 77 GCCTCCATATCAGCCGCGCTTATCTCATGCGCGTACCGGACACG 122
DB 791 GTTGCCACATTTGGCCATACCAATCTCAAGTCCAGAAAGTACAG 836
RESULT 10
ABL27502/c
ID ABL27502 standard; DNA; 3448 BP.
XX
AC ABL27502;
XX
DT 26-MAR-2002 (first entry)
XX
XX Drosophila melanogaster genomic polynucleotide SEQ ID NO 33979.
XX
XX Drosophila; developmental biology; cell signalling; insecticide;
XX pharmaceutical; gene; ds.
XX
XX Drosophila melanogaster.
XX
XX WO200171042-A2.
XX
XX 27-SEP-2001.
XX
XX 23-MAR-2001; 2001MO-US009231.
XX
XX 23-MAR-2000; 2000US-0191637P.
XX
XX 11-JUL-2000; 2000US-00614150.
XX
XX (PEKE) PE CORP NY.
XX
XX Venter JC, Adams M, Li PWD, Myers EW;
XX WPI; 2001-656860/75.
XX
XX New isolated nucleic acid detection reagent for detecting 1000 or more
XX genes from Drosophila and for elucidating cell signaling and cell-cell
XX interactions.
XX
XX Claim 1; SEQ ID NO 33979; 21pp + Sequence Listing; English.
XX
XX The invention relates to an isolated nucleic acid detection reagent
XX capable of detecting 1000 or more genes from Drosophila. The invention is
XX useful in developmental biology and in elucidating cell signaling and
XX cell-cell interactions in higher eukaryotes for the development of
XX insecticides, therapeutics and pharmaceutical drugs. The invention

CC discloses genomic DNA sequences (AB16176-AB130511), expressed DNA
CC sequences (AB101840-AB16175) and the encoded proteins (AB57737-
CC AB572072). The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 3448 BP; 894 A; 817 C; 801 G; 936 T; 0 U; 0 Other;
Query Match 17.4%; Score 30.8; DB 4; Length 3448;
Best Local Similarity 55.7%; Pred. No. 8.4;
Matches 59; Conservative 0; Mismatches 47; Indels 0; Gaps 0;
QY 17 ACCGCCAGCTTCCTGTGTTGCTAACCGGAGCCGAGCGAACTCTTATCGGAACAGACGC 76
DB 1667 ACAACAGCTTCCTGTGAGGTGCGCCACAGCGGGTCTTATGCGGCTCCGGTGC 1608
QY 77 GCCTCCATATCAGCCGCGCTTATCTCATGCGCGTACCGGACACG 122
DB 1607 GTTGCCACATTTGGCCATACCAATCTCAAGTCCAGAAAGTACAG 1562
RESULT 11
ABL18800/c
ID ABL18800 standard; DNA; 3600 BP.
XX
AC ABL18800;
XX
DT 26-MAR-2002 (first entry)
XX
XX Drosophila melanogaster genomic polynucleotide SEQ ID NO 7873.
XX
XX Drosophila; developmental biology; cell signalling; insecticide;
XX pharmaceutical; gene; ds.
XX
XX Drosophila melanogaster.
XX
XX WO200171042-A2.
XX
XX 27-SEP-2001.
XX
XX 23-MAR-2001; 2001MO-US009231.
XX
XX 23-MAR-2000; 2000US-0191637P.
XX
XX 11-JUL-2000; 2000US-00614150.
XX
XX (PEKE) PE CORP NY.
XX
XX Venter JC, Adams M, Li PWD, Myers EW;
XX WPI; 2001-656860/75.
XX
XX New isolated nucleic acid detection reagent for detecting 1000 or more
XX genes from Drosophila and for elucidating cell signaling and cell-cell
XX interactions.
XX
XX Claim 1; SEQ ID NO 7873; 21pp + Sequence Listing; English.
XX
XX The invention relates to an isolated nucleic acid detection reagent
XX capable of detecting 1000 or more genes from Drosophila. The invention is
XX useful in developmental biology and in elucidating cell signaling and
XX cell-cell interactions in higher eukaryotes for the development of
XX insecticides, therapeutics and pharmaceutical drugs. The invention
XX discloses genomic DNA sequences (AB16176-AB130511), expressed DNA
XX sequences (AB101840-AB16175) and the encoded proteins (AB57737-
XX AB572072). The sequence data for this patent did not form part of the
XX printed specification, but was obtained in electronic format directly
XX from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 3600 BP; 946 A; 856 C; 823 G; 975 T; 0 U; 0 Other;
Query Match 17.4%; Score 30.8; DB 4; Length 3600;
Best Local Similarity 55.7%; Pred. No. 8.5;
Matches 59; Conservative 0; Mismatches 47; Indels 0; Gaps 0;


```
QY 17 ACCGACCTTCTCTGTTGCTAACCGAGCCGAGCGAAGCTCTTATCGAAGACGACGC 76
DB 1667 ACAACACCTTCCGGTGGAGGCGCCACAGCGGGTCTTGTGGCGGCTCCGGTGGC 1608
QY 77 GCCTCCATATCAGCGCGCGCTTATCTCATGCGCGTGAACCGACAGC 122
DB 1607 GTTGGCACATTGGCCATACAAATCTCAAGTCCAGAAAGTACAAAG 1562

RESULT 12
AAD64735
ID AAD64735 standard; DNA; 29169 BP.
AC AAD64735;
XX
XX 11-MAR-2004 (first entry)
DT
XX Human carcinoma-associated (CA) gene TBX21.
DE
XX Carcinoma-associated protein; CAP; acinar cell carcinoma; fibrosarcoma;
KM Kaposi's sarcoma; breast cancer; Hairy cell leukaemia; human; ds.
XX Homo sapiens.
OS
XX US2003099963-A1.
PN
XX 29-MAY-2003.
PD
XX 20-MAR-2002; 2002US-00105613.
PF
XX 22-DEC-2000; 2000US-00747377.
PR 02-MAR-2001; 2001US-00798586.
PR 08-NOV-2001; 2001US-00052482.
XX
XX (MORR/) MORRIS D W.
PA (ENGSE/) ENGELHARD E K.
XX
XX Morris DW, Engelhard EK;
PI
XX WPI; 2003-874605/81.
DR
XX Novel recombinant carcinoma-associated protein such as mouse or human
PT TBX21 protein, useful for screening a bioactive agent capable of binding
PT to carcinoma associated protein, and for evaluating the effect of a
PT candidate carcinoma drug.
XX
XX Disclosure; SEQ ID NO 4; 0pp; English.
XX
XX The present invention relates to novel recombinant carcinoma-associated
XX protein (CAP) useful for screening a bioactive agent capable of binding
XX to carcinoma associated (CA) protein and for evaluating the effect of a
XX candidate carcinoma drug. The invention also describes the use of novel
XX compositions for use in screening methods and provides compositions and
XX methods associated with altered expression of TBX21 in cancer. Suitable
XX cancers which can be diagnosed or screened by the invention includes
XX acinar cell carcinoma, fibrosarcoma, Kaposi's sarcoma, breast cancer and
XX Hairy cell leukaemia. The present sequence is human carcinoma-associated
XX (CA) gene
XX
SQ Sequence 29169 BP; 5725 A; 7553 C; 7224 G; 8641 T; 0 U; 26 Other;
QY Query Match 17.4%; Score 30.8; DB 10; Length 29169;
DB Best Local Similarity 61.0%; Pred. No. 14;
Matches 50; Conservative 0; Mismatches 32; Indels 0; Gaps 0;
QY 11 GACAGAGCGGACGCTCTGTTGCTAACCGAGCGCGAAGCTCTTATCGAAGACA 70
DB 8982 GACACGACGCGCTCTCTCTGTGGGAACTGAGAGGAGAGCCCTTATCTCCGGG 9041
QY 71 GAGCGCGCTTCATATCAGCGC 92
DB 9042 CCCCCTGCGCCACCTCCCGC 9063
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```
RESULT 13
ADT47065
ID ADT47065 standard; cDNA; 1404 BP.
XX
XX ADT47065;
AC
XX 02-DEC-2004 (first entry)
DT
XX
XX Bacterial polynucleotide #21816.
DE
XX Recombinant DNA construct; transformed plant; improved plant property;
KM cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;
KM pathogen tolerance; pest tolerance; plant disease resistance;
KM cell cycle pathway modification; plant growth regulator;
KM homologous recombination; seed oil yield; protein yield; carbohydrate;
KM nitrogen; phosphorus; photosynthesis; lignin; galactomannan;
KM bacterial polynucleotide; gene; ss.
XX
XX Bacteria.
OS
XX US2003233675-A1.
PN
XX 18-DEC-2003.
PD
XX 20-FEB-2003; 2003US-00369493.
PF
XX 21-FEB-2002; 2002US-0360039P.
PR
XX
XX (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
XX
XX Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;
PI
XX WPI; 2004-061375/06.
DR
XX New recombinant DNA construct comprising a promoter positioned to provide
PT for expression of a polynucleotide encoding a polypeptide from a
PT microbial source, useful for producing plants with improved properties.
PT
XX
XX Claim 1; SEQ ID NO 45503; 122pp; English.
XX
XX The invention relates to a recombinant DNA construct comprising a
XX promoter functional in a plant cell, where the promoter is positioned to
XX provide for expression of a polynucleotide encoding a polypeptide from a
XX microbial source. The invention also relates to a transformed plant
XX comprising the recombinant DNA construct and a method of producing a
XX transformed plant having an improved property. The plant is a crop plant
XX such as maize or soybean. The method of producing a transformed plant
XX having an improved property comprises transforming a plant with the
XX recombinant DNA construct and growing the transformed plant, where the
XX polynucleotide or polypeptide is useful for improving plant properties.
XX The recombinant DNA construct is useful for producing plants with
XX improved plant properties, e.g. improved cold, heat or drought tolerance,
XX tolerance to herbicides, extreme osmotic conditions, pathogens or pests,
XX increased resistance to plant disease, better growth rate by modification
XX of the cell cycle pathway with plant growth regulators, increased rate of
XX homologous recombination, modified seed oil or protein yield and/or
XX phosphorus use and/or uptake, by modification of photosynthesis or by
XX providing improved plant growth and development under at least one stress
XX condition, improved lignin production or improved galactomannan
XX production. This sequence represents a bacterial polynucleotide used in
XX the scope of the invention. Note: The sequence data for this patent did
XX not form part of the printed specification but was obtained in electronic
XX format from USPTO at seqdata.uspto.gov/sequence.html.
XX
SQ Sequence 1404 BP; 236 A; 489 C; 454 G; 225 T; 0 U; 0 Other;
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Query Match          17.3%; Score 30.6; DB 13; Length 1404;
Best Local Similarity 62.3%; Pred. No. 7.9;
Matches 48; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

QY 99 ATCTCATGCGGTGACCGGACGAGCGCCGTCCTTATGCGGCTATAAATACAG 158
DB 464 ACCGCAAGGGGCTGAACGTGCCGATGTGTGTCGCCGCTTGCCGCTTTCCGCAAG 523
QY 159 CCGGCAACGATCTGTGTA 175
DB 524 ACCGCGACGATCTGGAA 540

RESULT 14
AEC75808
ID AEC75808 standard; DNA; 10968 BP.
AC AEC75808;
XX
XX
DT 01-DEC-2005 (first entry)
DE P. celluloseum ambruticin ambC gene.
KM de; gene; ambC; ambruticin; fungal infection; fungicide; polyketide.
XX Polyangium celluloseum.
OS WO2005086907-A2.
XX
XX PD 22-SEP-2005.
PF 08-MAR-2005; 2005WO-US007924.
XX
XX PR 08-MAR-2004; 2004US-0551103P.
PR 04-MAY-2004; 2004US-0568290P.
XX PR 07-MAR-2005; 2005US-00075185.
XX
XX PA (KOSA-) KOSAN BIOSCIENCES INC.
XX
XX PI Reeves CD, Julien B, Reid RC;
XX WPI; 2005-639088/65.
XX
XX PT New nucleic acids encoding polyketide synthases and polyketide
PT modification enzymes involved in or required for the biosynthesis of
PT ambruticin, useful for producing polyketides, e.g. ambruticins, for
PT treating fungal infections.
XX
XX PS Claim 4; SEQ ID NO 35; 2855bp; English.
XX
XX CC The invention relates to a purified or recombinant nucleic acid (I)
XX comprising a nucleotide sequence encoding a polypeptide involved in or
XX required for the biosynthesis of ambruticin. The complement of the
XX nucleotide sequence hybridizes to a nucleic acid encoding a domain
XX selected from beta-ketoacyl synthase, acyltransferase, beta-ketoreductase,
XX dehydratase, enoylreductase, or acyl carrier protein domains of the
XX Sorangium cellulosum (synonym: Polyangium celluloseum) ambruticin gene
XX cluster, or where the complement of the nucleotide sequence hybridizes to
XX a nucleic acid encoding an amino acid sequence selected from (SEQ ID NO.
XX 11-19 (AEC75784-AEC75792). The nucleic acid is useful for producing
XX polyketides, including ambruticins and ambruticin analogs and
XX derivatives. Ambruticins can be used for treating fungal infections. The
XX present sequence represents P. celluloseum ambruticin ambC gene.
XX
SQ Sequence 10968 BP; 1231 A; 3980 C; 4394 G; 1363 T; 0 U; 0 Other;

Query Match          17.3%; Score 30.6; DB 14; Length 10968;
Best Local Similarity 53.3%; Pred. No. 13;
Matches 88; Conservative 0; Mismatches 74; Indels 3; Gaps 1;

QY 3 CTATATGTAACAGAGCCGACCTTCTGTGTGTTGCTAACCGGACGCGACGCAACTCTTAA 62
DB 6775 CTCTCTCTGTGCGGTCCGACGAGCCGCGCTGCGCCGACGCGCGGCGGCTCGCC--- 6831

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QY 63 TCGGAACAGACGCGCTCCATATCAGCCGCGGTTATCTCATGCGGTGACCGGACAG 122
DB 6832 GAGACACTGCGCGCCACCGGACGAGCGGCTGCTGACCTGCCCGGAGACCTGGCCACG 6891
QY 123 AGCGCGCCGTCCTGCTTATGCGGCTATAAATACAGCCGCAAG 167
DB 6892 ACCGCGACGACCTCGGCAACGCGGCTCGCGCTCGCGCGCG 6936

RESULT 15
AEC75774
ID AEC75774 standard; DNA; 78869 BP.
AC AEC75774;
XX
XX
DT 01-DEC-2005 (first entry)
DE Polyangium celluloseum ambruticin biosynthetic gene cluster.
XX
XX KM de; ambruticin; fungal infection; fungicide; polyketide.
XX Polyangium celluloseum.
OS WO2005086907-A2.
XX
XX PD 22-SEP-2005.
PF 08-MAR-2005; 2005WO-US007924.
XX
XX PR 08-MAR-2004; 2004US-0551103P.
PR 04-MAY-2004; 2004US-0568290P.
XX PR 07-MAR-2005; 2005US-00075185.
XX
XX PA (KOSA-) KOSAN BIOSCIENCES INC.
XX
XX PI Reeves CD, Julien B, Reid RC;
XX WPI; 2005-639088/65.
XX
XX DR P-PSDB; AEC75776, AEC75777, AEC75778, AEC75779, AEC75780, AEC75781,
DR AEC75782, AEC75783, AEC75784, AEC75785, AEC75786, AEC75787, AEC75788,
DR AEC75789, AEC75790, AEC75791, AEC75792, AEC75801, AEC75802, AEC75803.
XX
XX PT New nucleic acids encoding polyketide synthases and polyketide
PT modification enzymes involved in or required for the biosynthesis of
PT ambruticin, useful for producing polyketides, e.g. ambruticins, for
PT treating fungal infections.
XX
XX PS Disclosure; SEQ ID NO 1; 2855bp; English.
XX
XX CC The invention relates to a purified or recombinant nucleic acid (I)
XX comprising a nucleotide sequence encoding a polypeptide involved in or
XX required for the biosynthesis of ambruticin. The complement of the
XX nucleotide sequence hybridizes to a nucleic acid encoding a domain
XX selected from beta-ketoacyl synthase, acyltransferase, beta-ketoreductase,
XX dehydratase, enoylreductase, or acyl carrier protein domains of the
XX Sorangium cellulosum (synonym: Polyangium celluloseum) ambruticin gene
XX cluster, or where the complement of the nucleotide sequence hybridizes to
XX a nucleic acid encoding an amino acid sequence selected from (SEQ ID NO.
XX 11-19 (AEC75784-AEC75792). The nucleic acid is useful for producing
XX polyketides, including ambruticins and ambruticin analogs and
XX derivatives. Ambruticins can be used for treating fungal infections. The
XX present sequence represents Polyangium celluloseum ambruticin biosynthetic
XX gene cluster.
XX
SQ Sequence 78869 BP; 10766 A; 27557 C; 28921 G; 11625 T; 0 U; 0 Other;

Query Match          17.3%; Score 30.6; DB 14; Length 78869;
Best Local Similarity 53.3%; Pred. No. 21;
Matches 88; Conservative 0; Mismatches 74; Indels 3; Gaps 1;

QY 3 CTATATGTAACAGAGCCGACCTTCTGTGTGTTGCTAACCGGACGCGACGCAACTCTTAA 62

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Db 22042 CTGCTCTGTGCGGGTCGAGACGACCGCGCTGCGCCGACGCGCGGCGCTCGCC--- 22098
QY 63 TCGGAACAGAGACGCGCCTCCATATCAGCCGCGCTTATCTCATGCGCGGTGACCGGACACG 122
Db 22099 GAGCACCCTGCGCGCGCCACCGGACGAGCGGCTGCTCGACGTGCGCGCGGACGCTGGCCACG 22158
QY 123 AGGCGCCCGTCCGCGCTTATGCGGCTATTAATACAGCCCGACAG 167
Db 22159 ACGCGACGACACTCGCCACGCGGCTGCGCTGCGCTGCGGCGCG 22203

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Job time : 192.921 secs

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GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: June 15, 2006, 16:32:06 ; Search time 1481.21 Seconds
(without alignments)
6682.184 Million cell updates/sec

Title: US-09-896-888a-1_COPY_351_527

Perfect score: 177
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapekt 1.0

Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

EST:*
1: gb_esc1:*
2: gb_esc3:*
3: gb_esc4:*
4: gb_esc5:*
5: gb_esc6:*
6: gb_esc7:*
7: gb_esc2:*
8: gb_esc8:*
9: gb_esc9:*
10: gb_esc10:*
11: gb_gsa1:*
12: gb_gsa2:*
13: gb_gsa3:*
14: gb_gsa4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	35.4	20.0	822	9	DN873866 nad29c08.
2	33.8	19.1	507	11	AQ297217 HS_2266_A
3	33.6	19.0	343	4	BY342594 BY342594
4	33.6	19.0	402	4	BY077721 BY077721
5	33.2	18.8	931	8	CV068875 f2_new.ch
6	33	18.6	348	4	BY338426 BY338426
7	33	18.6	353	4	BY337247 BY337247
8	33	18.6	354	4	BY013584 BY013584
9	33	18.6	355	4	BY340467 BY340467
10	33	18.6	360	4	BY343718 BY343718
11	33	18.6	362	4	BY339252 BY339252
12	33	18.6	371	4	BY083658 BY083658
13	33	18.6	611	5	CP916169 B0991A12-
14	33	18.6	621	5	B0620008 Tactr1386
15	33	18.6	624	5	CP913548 B0950D02-
16	33	18.6	635	7	AA918335 uc11f04.y
17	33	18.6	641	1	AA989838 uc79f07.y
18	33	18.6	657	5	CF915946 B0987F04-
19	33	18.6	669	5	CF174622 B0941F09-

20	33	18.6	973	4	CA490927	CA490927
21	33	18.6	1029	13	CM919246	CM919246
22	33	18.6	1987	6	AK144659	AK144659
23	32.8	18.5	617	13	CM192940	CM192940
24	32.8	18.5	638	12	CE066545	CE066545
25	32.6	18.4	786	13	CL421872	CL421872
26	32.4	18.3	636	8	CO973145	CO973145
27	32	18.1	327	4	BY789720	BY789720
28	32	18.1	1297	4	BQ645920	BQ645920
29	31.8	18.0	553	8	CR540072	CR540072
30	31.8	18.0	1076	4	BX463482	BX463482
31	31.8	18.0	3592	6	CR859367	CR859367
32	31.6	17.9	681	14	DX006812	DX006812
33	31.6	17.9	1011	13	CL494562	CL494562
34	31.6	17.9	1310	3	BQ720271	BQ720271
35	31.4	17.7	344	4	BY340052	BY340052
36	31.4	17.7	361	5	CJ079027	CJ079027
37	31.4	17.7	374	7	BB843476	BB843476
38	31.4	17.7	392	5	CJ086368	CJ086368
39	31.4	17.7	681	12	CG295117	CG295117
40	31.2	17.6	543	5	CK071906	CK071906
41	31.2	17.6	595	5	CK066979	CK066979
42	31.2	17.6	665	13	CM170205	CM170205
43	31.2	17.6	666	13	CM502443	CM502443
44	31.2	17.6	693	12	CL190317	CL190317
45	31.2	17.6	787	13	CM028427	CM028427

ALIGNMENTS

RESULT 1
DN873866 822 bp mRNA linear EST 21-Apr-2005
nad29c08.y1 Dog eye cornea. Unnormalized (nad) Canis familiaris
LOCUS
DEFINITION
CDNA clone nad29c08 5', mRNA sequence.
ACCESSION
DN873866
VERSION
DN873866.1 GI:62843807
KEYWORDS
EST,
SOURCE
Canis familiaris (dog)
ORGANISM
Canis familiaris
Eukaryotes; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
Canis.

REFERENCE
1 (bases 1 to 822)
Wistow,G.
AUTHORS
NEIBank analysis of Dog cornea
TITLE
Unpublished (2005)
JOURNAL
COMMENT
Contact: Wistow G
Section on Molecular Structure and Function
National Eye Institute
6/331, NIH, Bethesda, MD 20892-2740, USA
Tel: 301 402 3452
Fax: 301 496 0078
Email: graeme@helix.nih.gov
Plate: 29 row: c column: 08
Seq primer: Universal M13 Reverse.
Location/Qualifiers
1. 822

FEATURES
source
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/strain="Beagle"
/db_xref="taxon:9615"
/clone="nad29c08"
/issue_type="Cornea"
/dev_stage="Adult"
/lab_pos="EMDH108"
/clone_lib="Dog eye cornea. Unnormalized (nad)"
/note="Organ: Eye; Vector: pCMVSPORT6; RNA was extracted from dog cornea tissue. A directionally cloned cDNA library in the pCMVSPORT6 vector (Invitrogen) was constructed at Bioserve Biotechnology (Laurel MD) essentially following the protocols of the Superscript

Plasmid System, full details of which are contained in the manufacturer's instruction manual (<http://www.lifetechn.com/>). First strand synthesis was carried out using a Not I primer-adaptor (5'-pGACTGATCTCATGCGCGCGCCG(T)15-3'). cDNA was cloned in Not I/Sal I sites. EST analysis was performed at the NIH Intramural Sequencing Center (NISC). Analyzed data available through <http://neibank.nhl.nih.gov>.

ORIGIN

Query Match 20.0%; Score 35.4; DB 9; Length 822;

Best Local Similarity 54.1%; Pred. No. 2.4;

Matches 72; Conservative 0; Mismatches 61; Indels 0; Gaps 0;

QY 13 CAGAGCCGACCTTCTGTGTTGCTAACCGGACCGCACTCTTATCGAAGCAG 72
 DB 81 CAGGCGCCGACGATCACTGTGCCCCGAAACACCGCGCTGCGCCCTCCGCGCGCG 140
 QY 73 ACGGCGCTCCATATCAGCGCGCGTTATCTCATGCGCGTACCGGACGAGCGCGCGT 132
 DB 141 CTTCGCCGACTTCTCCGCTCGAGCTCTCCAGCGCGCGGATCTCTTGACCGGTCCT 200
 QY 133 CCGCGTTATCGCG 145
 DB 201 CCAGATTCGCGCG 213

RESULT 2

LOCUS AQ297217 507 bp DNA linear GSS 15-DEC-1998

DEFINITION HS 2266 A1 A08 MR CIT Approved Human Genomic Sperm Library D Homo

sequence genomic clone Plate=2266 Col=15 Row=A, genomic survey

ACCESSION AQ297217.1 GI:4014396

VERSION AQ297217.1

KEYWORDS GSS.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Hominidae; Homo.

1 (bases 1 to 507)

Mahatras,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,

Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and

Hood,L.

Sequence-tagged connectors: A sequence approach to mapping and

scanning the human genome

Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)

10449764

Contact: Mahatras GG, Wallace JC, Hood L

High Throughput Sequencing Center

University of Washington

401 Queen Anne Avenue North, Seattle, WA 98109, USA

Tel: (206) 616-3618

Fax: (206) 616-3887

Email: jwallace@u.washington.edu

Sequence Tagged Connector

Plate: 2266 row: A column: 15

Class: BAC ends

High quality sequence spot: 507.

FEATURES

source

1. 507

/organism="Homo sapiens"

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/db_xref="taxon:9606"

/clone="Plate=2266 Col=15 Row=A"

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/note="Organ: sperm; Vector: pBelobAC11, BAC Clones in

E-Coli DH10B"

Best Local Similarity 53.4%; Pred. No. 7.6;

Matches 71; Conservative 0; Mismatches 62; Indels 0; Gaps 0;

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 DB 106 TTCTTTAGTACACCCCTACCTCATCTGTGTGGATGAGATCCGCTATACCCCTTATG 165
 QY 65 GGACAGGAGCGCCCTCCATATCAGCGCGCGCTTATCTCATGCGCGTACCGGACCGAG 124
 DB 166 GGACAGGCGCTTCCAAACCACTGCTGCGCCAGAGAAACATGACCGCATTTCAACCAAT 225
 QY 125 GCGCGCGTCCCGC 137
 DB 226 GTCACTGTCTCTC 238

RESULT 3

LOCUS BY342594

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

1 (bases 1 to 343)

Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S.,

Nikaido,I., Osato,N., M., Saito,R., Suuki,H., Yamana,A.,

Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A.,

Schondach,C., Gojodori,T., Balderelli,R., Hill,D.P., Bult,C.,

Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapi,D., Matsuda,H.,

Batalov,S., Beisel,K.W., Blake,J.A., Brad,D., Brusan,Y.,

Choitha,C., Corbani,L.E., Cousins,S., Dalla,E., Dugan,T.A.,

Fletcher,C.F., Forrest,A., Frazer,K.S., Gaasterland,T.,

Gariboldi,M., Gissi,C., Godzik,A., Gough,J., Grimmond,S.,

Gastlrich,S., Hirokawa,N., Jackson,I.J., Jarvie,E.D., Kanai,A.,

Kawaji,H., Kawasawa,Y., Kedzierski,R.M., King,B.L., Konagaya,A.,

Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons,P.A., Maglott,D.R.,

Maltais,L., Marchionni,L., McKenzie,L., Miki,H., Nagashima,T.,

Numata,K., Okido,T., Pavan,W.J., Petrea,G., Pesole,G.,

Petrovsky,N., Pillai,R., Pontius,J.U., Qi,D., Ramchandran,S.,

Ravasi,T., Reed,J.C., Reed,D.J., Reid,J., Ring,B.Z., Ringwald,M.,

Sandelin,A., Schneider,C., Semple,C.A., Setou,M., Shimada,K.,

Sultana,R., Takekawa,Y., Taylor,M.S., Teasdale,R.D., Tomita,M.,

Verardo,R., Wagner,L., Wahlstedt,C., Wang,Y., Watanabe,Y.,

Welle,C., Wilming,L.G., Wrynshaw-Boris,A., Yanagisawa,M., Yang,I.,

Yang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A., Carninci,P.,

Hayatsu,N., Hirozane-Kishikawa,T., Kono,H., Nakamura,M.,

Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,T., Aizawa,K.,

Arakawa,T., Fukuda,S., Hara,A., Hashizume,W., Imotani,K., Ishii,Y.,

Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata,K.,

Shingawa,A., Yasuniishi,A., Yoshino,M., Waterston,R., Lander,E.S.,

Rogers,J., Birney,E. and Hayashizaki,Y.

Analysis of the mouse transcriptome based on functional annotation

of 60,770 full-length cDNAs

Nature 420, 563-573 (2002)

12466851

Contact: Yoshihide Hayashizaki

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The Institute of Physical and Chemical Research (RIKEN)

1-7-22 Suenho-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan

Tel: 81-45-503-9222

Fax: 81-45-503-9216

Email: genome-resgsc.riken.jp, <http://genome.gsc.riken.jp/>

Aizawa,K., Akinura,T., Arakawa,T., Carninci,P., Fukuda,S.,

Hirozane,T., Imotani,K., Ishii,Y., Itoh,M., Kawai,T., Kono,H.,

Miyazaki,A., Murata,M., Nakamura,M., Nomura,K., Numazaki,R.,

Ohno,M., Sakai,K., Sakazume,N., Sasaki,D., Sato,K., Shibata,K.,

Shingawa,A., Shiraki,T., Waki,K., Kawai,T., Aizawa,K.,

Arakawa,T., Fukuda,S., Hara,A., Hashizume,W., Imotani,K., Ishii,Y.,

Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata,K.,

Shingawa,A., Yasuniishi,A., Yoshino,M., Waterston,R., Lander,E.S.,

ORIGIN

Query Match 19.1%; Score 33.8; DB 11; Length 507;

Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Jarvis, E.D., Kanaï, A., Gustincich, S., Hirokawa, N., Jackson, I.J., Jarvis, E.D., Kanaï, A., Kawai, H., Kawasawa, Y., Kezizarski, R.M., King, B.L., Konagaya, A., Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maglot, D.R., Malats, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T., Numata, K., Okido, T., Pavan, M.J., Perce, G., Pesole, G., Petrovsky, N., Pillai, R., Pontius, J.U., Qi, D., Ramchandran, S., Ravasi, T., Reed, J.C., Reed, D.J., Reid, J., Ring, B.Z., Ringwald, M., Sadelain, A., Schneider, C., Sempile, C.A., Setou, M., Shimada, K., Sultana, R., Takenaka, Y., Taylor, M.S., Teasdale, R.D., Tomita, M., Verardo, R., Wagner, L., Wanstedt, C., Wang, Y., Watanabe, Y., Wells, C., Wilming, L.G., Wysshaw-Bois, A., Yanagisawa, M., Yang, I., Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P., Hayatsu, N., Hirozane-Kishikawa, T., Komno, H., Nakamura, R., Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K., Aizawa, T., Fukuda, S., Hara, A., Hashizume, W., Imocani, K., Ishii, Y., Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Saeki, D., Shibata, K., Shingawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S., Rogers, J., Birney, E. and Hayashizaki, Y.

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Nature 420, 563-573 (2002)

1246851

**JOURNAL
PUBLISHED**

COMMENT

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The Institute of Physical and Chemical Research (RIKEN)
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Email: genome-resgsc.riken.jp, URL: http://genome.gsc.riken.jp/
Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S., Hirozane, T., Imocani, K., Ishii, Y., Itoh, M., Kawai, J., Komno, H., Miyazaki, A., Murata, M., Nakamura, M., Nomura, K., Numazaki, R., Ohno, M., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shibata, K., Shiraki, T., Tagami, M., Waki, K., Watanabe, A., Muramatsu, M. and Hayashizaki, Y. Direct Submissions
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Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
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Please visit our web site (<http://genome.gsc.riken.go.jp>) for further details.

FEATURES

SOURCE

Location/Qualifiers

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/accession="G57BL/6J"

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f2_new_chopped.fasta.Contig488 Preamplified custom cDNA library in
pcwvspor6.1 (ResGen, Invitrogen Inc.) Emiliania huxleyi cDNA, mRNA
sequence.
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VERSION   CV068875.1 GI:51532039
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SOURCE    Emiliania huxleyi
ORGANISM  Emiliania huxleyi
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AUTHORS   Eukaryota; Haptophyceae; Isochrysidales; Emiliania.
TITLE     Wahlund,T.W., Zhang,X. and Read,B.A.
JOURNAL   Expressed Sequence Tag Profiles from Calcifying and Non-Calcifying
COMMENT   Cultures of Emiliania huxleyi
Microaleontology (2004) In press
Contact: Betsy Read
Department of Biological Sciences
California State University San Marcos
333 S. Twin Oaks Valley Road, San Marcos, CA 92036-0001, USA
Tel.: 760 750 4129
Email: bread@csusm.edu.

FEATURES
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RESULT 6

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BY338426 RIKEN full-length enriched, whole joints Mus musculus cDNA
clone L230014G21 5', mRNA sequence.
ACCESSION BY338426
VERSION   BY338426.1 GI:26534820
KEYWORDS  EST.
SOURCE    Mus musculus (house mouse)
ORGANISM  Mus musculus
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
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REFERENCE

1 (bases 1 to 348) Sciurognathi: Muroidea; Muridae; Murinae; Mus.

AUTHORS

Okazaki, I., Furuno, M., Kasukawa, T., Aichi, J., Bono, H., Kondo, S.,
 Nikaide, I., Osato, N., Saito, R., Suuki, H., Yamakata, I.,
 Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A.,
 Schombach, C., Gojobori, T., Balderelli, R., Hill, D.P., Balt, C.,
 Hume, D.A., Quackenbush, J., Schriml, L.M., Kanapin, A., Matsuda, H.,
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JOURNAL

12466851
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 Fax: 81-45-503-9216

COMMENT

Email: genome-resgsc.riken.jp, URL: http://genome.gsc.riken.jp/
 Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S.,
 Hirozane, T., Imotani, K., Ishii, Y., Itch, M., Kawai, J., Konno, H.,
 Miyazaki, A., Morita, M., Nakamura, M., Nomura, K., Nunazaki, R.,
 Ohno, M., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shibata, K.,
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 cDNA library was prepared and sequenced in Mouse Genome
 Encyclopedia Project of Genome Exploration Research Group in Riken
 Genomic Sciences Center and Genome Science Laboratory in Riken
 Division of Experimental Animal Research in Riken contributed to
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 Tissues were provided by Vassilis Adinola (Biomedical Sciences
 Research Center "Al. Fleming" Institute of Immunology 14-16 Al.
 Fleming street 16672 Vathi, Greece) whose assistance we gratefully
 acknowledge.
 Please visit our web site (http://genome.gsc.riken.go.jp) for
 further details.

FEATURES

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Source
location/Qualifiers
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DEFINITION BY337247 RIKEN full-length enriched, whole joints Mus musculus cDNA
ACCESSION BY337247
VERSION BY337247.1 GI:26532790
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Muridae; Murinae; Mus.
1 (bases 1 to 353)
Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S.,
Nikaido, R., Otsu, N., Saito, R., Suzuki, H., Yamana, T.,
Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A.,
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Hume, D. A., Quackenbush, J., Schiraldi, L. M., Kanapin, A., Matsuda, H.,
Batalov, S., Beisel, K. W., Blake, J. A., Brady, D., Brusic, V.,
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Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P.,
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Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K.,
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Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S.,
Hirozane, T., Imotani, K., Ishii, Y., Itoh, M., Kawai, J., Kono, H.,
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Research Center 'Al. Fleming' Institute of Immunology 14-16 Al.
Fleming street 16672 Vail, Greece) whose assistance we gratefully
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FEATURES
SOURCE
Location/Qualifiers
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ORIGIN
Query Match      18.6%; Score 33; DB 4; Length 353;
Best Local Similarity 51.7%; Pred. No. 13;
Matches 75; Conservative 0; Mismatches 70; Indels 0; Gaps 0;

Qy 3 CTTATCGTGACAGACGCCAGCTTCCTGTGTCTTAACCGACGCGGACGCAACTCCTTA 62
Db CTTATGTGATGCCCGCCCTTCTTCTTCGAGCTGACGCGGACGAGCGCGCTTT 158

Qy 63 TCGGAACAGACGCGGCTTCATATCAGCGCGGCTTATCTATGCGCTGACGACAGC 122
Db 159 CCTACACAGCTTCGACCTCTCCGCGGCGGACGAGCGCTCGCTCCCTGCCACACAGC 218

Qy 123 AGGCGCCGCTCCGCTTATCGCGCC 147
Db 219 GACAGAGCGCTCCGCTTCTCTTCC 243

RESULT 8
LOCUS BY013584 354 bp mRNA linear EST 06-DEC-2002
DEFINITION BY013584 RIKEN full-length enriched, lung RCB-0558 LLC cDNA Mus
ACCESSION BY013584
VERSION BY013584.1 GI:26073833
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Muridae; Murinae; Mus.
1 (bases 1 to 354)
Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S.,

```

Nikaido, I., Osato, N., Saito, R., Suzuki, H., Yamana, K., I., Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schombach, C., Gojobori, T., Baldarelli, R., Hill, D. P., Bull, C., Hume, D. A., Quackenbush, J., Schriml, L. M., Kanapin, A., Matsuda, H., Batalov, S., Beisel, K. W., Blake, J. A., Brad, D., Brusci, V., Chothia, C., Corbani, L. E., Cousins, S., Dalla, E., Dragani, T. A., Fletcher, C. F., Forrest, A., Frazer, K. S., Gaasterland, T., Gerbaldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S., Gustincich, S., Hirokawa, N., Jackson, I. J., Jarvis, E. D., Kanai, A., Kawaji, H., Kawasawa, Y., Kedzierski, R. M., King, B. L., Konagaya, A., Kurochkin, I. V., Lee, Y., Lenhard, B., Lyons, P. A., Maglott, D. R., Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T., Numa, K., Okido, T., Pavan, W. J., Pertea, G., Pesole, G., Petrovsky, N., Pillai, R., Pontius, J. U., Qi, D., Ramachandran, S., Ravasi, T., Reed, J. C., Reed, D. J., Reid, J., Ring, B. Z., Ringwald, M., Sandelin, A., Schneider, C., Semple, C. A., Setou, M., Shimada, K., Sultana, R., Takenaka, Y., Taylor, M. S., Teasdale, R. D., Tomita, M., Varrault, R., Wagner, L., Wahlestedt, C., Wang, Y., Watanabe, Y., Wells, C., Wilming, L. G., Wyszynski, B. S., Yang, A., Yanagisawa, M., Yang, I., Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P., Hayatsu, N., Hirozane-Kishikawa, T., Kono, H., Nakamura, M., Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K., Akakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K., Shingawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E. S., Rogers, J., Birney, E. and Hayashizaki, Y.

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JOURNAL PUBMED COMMENT

TITLE

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Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
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FEATURES

source
Location/Qualifiers
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/clone="G730040E06"
/tissue_type="lung"
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/clone_1nb="RIKEN full-length enriched, lung RCB-0558 LLC cDNA"

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Best Local Similarity 51.7%; Pred. No. 13;
Matches 75; Conservative 0; Mismatches 70; Indels 0; Gaps 0;

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Dy 116 CTTAAATGTATCCCGCCCGCTTCTTCTCGTAGCTGACGCGGACGACCGCTT 175
Qy 63 TCGGAACAGACCGCGCTCATATCAGCGCGGTTATCTCAGCCCGTACCGGACAG 122
Dy 176 CTTACACAGCTTCACACTCTCTCGGAGGCGACAGCTCGCGCTTCCACCAAG 235
Qy 123 AGGCGCCGCTCCGCTTATCGCGCC 147
Dy 236 GACAGACGCTCCCGCTTCCCTTCC 260

RESULT 9
BY340467
LOCUS
DEFINITION
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VERSION
KEYWORDS
SOURCE
ORGANISM

BY340467 355 bp mRNA linear EST 12-DEC-2002
BY340467 RIKEN full-length enriched, whole joints Mus musculus cDNA
clone U230028H13 5', mRNA sequence.
BY340467
BY340467.1 GI:26569955
EST.
Mus musculus (house mouse)
Mus musculus
Bkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 355)
Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Nikaido, I., Osato, N., Saito, R., Suzuki, H., Yamana, K., I., Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schombach, C., Gojobori, T., Baldarelli, R., Hill, D. P., Bull, C., Hume, D. A., Quackenbush, J., Schriml, L. M., Kanapin, A., Matsuda, H., Batalov, S., Beisel, K. W., Blake, J. A., Brad, D., Brusci, V., Chothia, C., Corbani, L. E., Cousins, S., Dalla, E., Dragani, T. A., Fletcher, C. F., Forrest, A., Frazer, K. S., Gaasterland, T., Gerbaldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S., Gustincich, S., Hirokawa, N., Jackson, I. J., Jarvis, E. D., Kanai, A., Kawaji, H., Kawasawa, Y., Kedzierski, R. M., King, B. L., Konagaya, A., Kurochkin, I. V., Lee, Y., Lenhard, B., Lyons, P. A., Maglott, D. R., Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T., Numa, K., Okido, T., Pavan, W. J., Pertea, G., Pesole, G., Petrovsky, N., Pillai, R., Pontius, J. U., Qi, D., Ramachandran, S., Ravasi, T., Reed, J. C., Reed, D. J., Reid, J., Ring, B. Z., Ringwald, M., Sandelin, A., Schneider, C., Semple, C. A., Setou, M., Shimada, K., Sultana, R., Takenaka, Y., Taylor, M. S., Teasdale, R. D., Tomita, M., Varrault, R., Wagner, L., Wahlestedt, C., Wang, Y., Watanabe, Y., Wells, C., Wilming, L. G., Wyszynski, B. S., Yang, A., Yanagisawa, M., Yang, I., Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P., Hayatsu, N., Hirozane-Kishikawa, T., Kono, H., Nakamura, M., Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K., Akakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K., Shingawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E. S., Rogers, J., Birney, E. and Hayashizaki, Y.

TITLE

JOURNAL PUBMED COMMENT

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Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S., Hirozane, T., Imotani, K., Ishii, Y., Itoh, M., Kawai, J., Kono, H.,

Myazaki, A., Murata, M., Nakamura, M., Nomura, K., Numata, K., Ohno, M., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shibata, K., Shiraki, T., Tagami, M., Waki, K., Watahiki, A., Muramatsu, M., and Hayashizaki, Y. Direct Submission

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Tissues were provided by Vassilis Aidinis (Biomedical Sciences Research Center 'Al. Fleming' Institute of Immunology 14-16 Al. Fleming street 16672 Vari, Greece) whose assistance we gratefully acknowledge.

Please visit our web site (<http://genome.gsc.riken.go.jp>) for further details.

Location/Qualifiers

1. 355

/organism="Mus musculus"

/mol_type="mRNA"

/db_xref="taxon:10090"

/clone="L230028H13"

/tissue_type="whole joints"

/clone_lib="RIKEN full-length enriched, whole joints"

ORIGIN

Query Match 18.6%; Score 33; DB 4; Length 355;

Best Local Similarity 51.7%; Pred. No. 13;

Matches 75; Conservative 0; Mismatches 70; Indels 0; Gaps 0;

QY 3 CTTATCGTACAGAGCGCGCTTCTGTGTCTTAACCGAGCGGACGACTCTT 62

DB 99 CTTAATGTGATCCCGCCCCCTTCTCTCCCTACGACCGGAGAGCGGCTT 158

QY 63 TCGGAACAGAGCGCGCTCATATACCGCGCTTATCTCAGCGGCTACCGGACAGC 122

DB 159 CTTACAGAGCTCGACCTCTCTCGGGGCGACGCGCTCGCGCTCCCTCCACACG 218

QY 123 AGGCGCGCTCGCGCTTATCGCGC 147

DB 219 GACAGAGCGTCCGCTTCCCTCC 243

RESULT 10 360 bp mRNA linear EST 12-DEC-2002

BY343718 RIKEN full-length enriched, whole joints Mus musculus cDNA

LOCUS clone L230047A12 5', mRNA sequence.

DEFINITION

ACCESSION BY343718

VERSION BY343718.1 GI:26573206

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

ORGANISM

Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathu; Muridae; Muridae; Murinae; Mus.

1 (bases 1 to 360)

Ohtsaki, Y., Furuno, M., Kaenkawa, T., Adachi, J., Bono, H., Kondo, S., Nishida, I., Otsu, N., Saito, R., Suzuki, H., Yamana, I., Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schombach, C., Gojodori, T., Baldarelli, R., Hill, D. P., Bull, C., Hume, D. A., Quackenbush, J., Schriml, L. M., Kanapin, A., Matsuda, H., Batalov, S., Beisel, K. W., Blake, J. A., Brad, D., Brusic, V.,

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Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

Nature 420, 563-573 (2002)

12466851

JOURNAL

PUBMED

COMMENT

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Fax: 81-45-503-9216

Email: genome-res@sc.riken.jp, URL: <http://genome.gsc.riken.jp/>

Aizawa, K., Akimura, T., Aizawa, T., Carninci, P., Fukuda, S., Hirozane, T., Imotani, K., Ishii, Y., Itoh, M., Kawai, J., Komori, H., Miyazaki, A., Murata, M., Nakamura, M., Nomura, K., Numata, K., Ohno, M., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shibata, K., Shiraki, T., Tagami, M., Waki, K., Watahiki, A., Muramatsu, M. and Hayashizaki, Y. Direct Submission

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Tissues were provided by Vassilis Aidinis (Biomedical Sciences Research Center 'Al. Fleming' Institute of Immunology 14-16 Al. Fleming street 16672 Vari, Greece) whose assistance we gratefully acknowledge.

Please visit our web site (<http://genome.gsc.riken.go.jp>) for further details.

Location/Qualifiers

1. 360

/organism="Mus musculus"

/mol_type="mRNA"

/db_xref="taxon:10090"

/clone="L230047A12"

/tissue_type="whole joints"

/clone_lib="RIKEN full-length enriched, whole joints"

ORIGIN

Query Match 18.6%; Score 33; DB 4; Length 360;

Best Local Similarity 51.7%; Pred. No. 13;

Matches	75; Conservative	0; Mismatches	70; Indels	0; Gaps	0;
Qy	3 CTTATCTGACAGAGCGCCAGCTTCTCTGTGTGCTAACCGAGCGGACGAACTCTTA 62				
Db	99 CTTAATGTGATCCCCCCCCCTTTCTTTCTCCGTAGCTGACCGGACGAGCGCGTTT 158				
Qy	63 TCGGAACAGAGCGCGCTTCATATCAGCCGCGCTTATCTCATGCGGCTGACCGAGACG 122				
Db	159 CTCACACAGCTCGACACTCTCTCGGGGGCGGACCGCTCGCTCCCTCTGCCACACG 218				
Qy	123 AGCGCCCGCTCCGCTTATCGCGC 147				
Db	219 GACAGAGCGTCCCGCTTCCCTCTCC 243				
RESULT 11	BY339252 362 bp mRNA linear EST 12-DEC-2002				
BY339252	BY339252 RIKEN full-length enriched, whole joints Mus musculus cDNA				
DEFINITION	clone l230021B07 5', mRNA sequence.				
ACCESSION	BY339252				
VERSION	BY339252.1 GI:26568740				
KEYWORDS	EST.				
ORGANISM	Mus musculus (house mouse)				
SOURCE	Mus musculus				
REFERENCE	Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muroidea; Muridae; Murinae; Mus.				
AUTHORS	1 (bases 1 to 362) Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Nkaido, I., Osato, N., Saito, R., Suzuki, H., Yamana, I., Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schombach, C., Gojbori, T., Baldarelli, R., Hill, D. P., Bult, C., Hume, D. A., Quackenbush, J., Schriml, L. M., Kanapin, A., Matsuda, H., Batalov, S., Beisel, K. W., Blake, J. A., Bradt, D., Brusc, V., Chothia, C., Corbani, L. E., Cousins, S., Dalla, E., Dragani, T. A., Fletcher, C. F., Forrest, A., Frazer, K. S., Gaasterland, T., Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimond, S., Gustinch, S., Hirokawa, N., Jackson, I. J., Jarvis, E. D., Kanai, A., Kawaji, H., Kawasawa, Y., Kedzierski, R. M., King, B. L., Konagaya, A., Korochkin, I. V., Lee, Y., Lenhard, B., Lyons, P. A., Maglott, D. R., Maita, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T., Numata, K., Okido, T., Pavan, W. J., Pertea, G., Pesole, G., Petrovsky, N., Pillai, R., Pontius, J. U., Qi, D., Ramchandran, S., Ravasi, T., Reed, J. C., Reed, D. J., Reid, J., Ring, B. Z., Ringwald, M., Sanderlin, A., Schneider, C., Semp, C. A., Setou, M., Shimada, K., Sultana, R., Takenaka, Y., Taylor, M. S., Teasdale, R. D., Tomita, M., Verardo, R., Wagner, L., Wahlstedt, C., Wang, Y., Watanabe, Y., Wells, C., Wilming, L. G., Wyszynski, B. A., Yanagisawa, M., Yang, I., Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P., Hayatsu, N., Hirozane-Kishikawa, T., Kono, H., Nakamura, M., Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Atawa, K., Ataka, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K., Shingawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E. S., Rogers, J., Birney, B. and Hayashizaki, Y.				
TITLE	Analysis of the mouse transcriptome based on functional annotation				
JOURNAL	Nature 420, 563-573 (2002)				
COMMENT	12466851 Contact: Yoshihide Hayashizaki Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute The Institute of Physical and Chemical Research (RIKEN) 1-7-22 Suenho-cho, Tsurumi-Ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9222 Fax: 81-45-503-9216 Email: genome-res@sc.riken.jp, URL: http://genome.gsc.riken.jp/ Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S., Hirozane, T., Imotani, K., Ishii, Y., Itoh, M., Kawai, J., Kono, H., Miyazaki, A., Murata, M., Nakamura, M., Nomura, K., Numazaki, R., Ohno, M., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shibata, K., Shiraki, T., Tagami, M., Waki, K., Watanabe, A., Muramatsu, M. and				

FEATURES	source				
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VERSION	/tissue_type="whole joints"				
KEYWORDS	/clone_1ib="RIKEN full-length enriched, whole joints"				
ORGANISM	Mus musculus (house mouse)				
SOURCE	Mus musculus				
REFERENCE	Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.				
AUTHORS	1 (bases 1 to 371) Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Nkaido, I., Osato, N., Saito, R., Suzuki, H., Yamana, I., Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schombach, C., Gojbori, T., Baldarelli, R., Hill, D. P., Bult, C., Hume, D. A., Quackenbush, J., Schriml, L. M., Kanapin, A., Matsuda, H., Batalov, S., Beisel, K. W., Blake, J. A., Bradt, D., Brusc, V., Chothia, C., Corbani, L. E., Cousins, S., Dalla, E., Dragani, T. A., Fletcher, C. F., Forrest, A., Frazer, K. S., Gaasterland, T., Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimond, S.,				

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Location/Qualifiers
1. 371
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="RG30044113"
/tissue_type="heart"
/dev_stage="10 days neonate"
/clone_lib="RIKEN full-length enriched, 10 days neonate heart"

ORIGIN

Query Match 18.5%; Score 33; DB 4; Length 371;
Best Local Similarity 51.7%; Pred. No. 13;
Matches 75; Conservative 0; Mismatches 70; Indels 0; Gaps 0;
3 CTTATCGTACAGAGCCGACCTTCCTGTGCTTACCGCAGCGACCACTCTTA 62
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 111 CTTATGATGATCCCGCCCCCTTCTCTCTCGGTAGCCGAGCGGACAGCCGCTT 170
Cy 63 TCGAATGAGAGCGGCGCTTCATATGACCGCGGTATTCATGCGGTACCGAGACG 122
Db 171 CTTACACGAGCTCGGACCTCTCTCGGCGGCGCAGCGCTCGCGCTCCACACG 230
Cy 123 AGGCGCGCGCGCGCTTATGCGCGC 147
Db 231 GACAGAGCGTCCGCTTCCTCTCC 255

RESULT 13
CP916169
LOCUS 611 bp mRNA linear EST 05-NOV-2003
DEFINITION B0991A12-5 NIA Mouse Unfertilized Egg cDNA Library (Long 1) Mus musculus cDNA clone NIA:B0991A12 IMAGE:30480971 5', mRNA sequence.
CP916169
VERSION CP916169.1 GI:38187371
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 611)
Piao, Y., Ko, N. T., Lim, M. K., and Ko, M. S. H.
Construction of long-transcript enriched cDNA libraries from submicrogram amounts of total RNAs by a universal PCR amplification method
Genome Res. 11 (9), 1553-1558 (2001)

JOURNAL PUBLISHED

CONTACT: Dawood B. Dudekula
Laboratory of Genetics
National Institute on Aging/National Institutes of Health
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
Email: cdna@nigun.grc.nia.nih.gov
Seq primer: M13 Reverse
High quality sequence stop: 611
POLYA=No.

FEATURES source

Location/Qualifiers
1. 611
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="nlaEST:B0991A12-5"
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/lab_host="DH10B"
/clone_lib="NIA Mouse Unfertilized Egg cDNA Library (Long 1)"
/note="Vector: pCMV-SPORT6 (Invitrogen); Site 1: SalI; Site 2: NotI; Mouse cDNA project by the Laboratory of Genetics, National Institute on Aging (NIA), Intramural Research Program, NIH (http://lgsun.grc.nia.nih.gov/cDNA). This is a long-transcript enriched cDNA library (Ref. Genome Res. 11: 1553-1558 (2001)). [PMID: 11544199]". Total RNAs were extracted from a pool of 1488 unfertilized eggs. Double-stranded cDNAs were synthesized with an Oligo(dT) primer [Invitrogen: 5'-pGACTAGTTCATGATCGCAGCGCGCCCTTTT-3'], treated with T4 DNA polymerase, and purified by ethanol-precipitation. The cDNAs were ligated to lone-linker L1-SalI, purified by phenol/chloroform, and separated from free linkers by Centricon 100. Then, the cDNAs were amplified by long-range high fidelity PCR using Ex Taq polymerase (Takara) with a primer SalI-S. The products were purified by phenol/chloroform and Centricon 100. The cDNAs were digested with SalI and NotI enzymes and cloned into SalI/NotI site of pCMV-SPORT6 plasmid vector. The DH10B E. coli host was transformed with the ligation mixture by the standard chemical method. The

average insert size is about 2.5 kb. The library was constructed by Yulan Piao."

Query Match	18.6%	Score 33	DB 5	Length 624
Best Local Similarity	51.7%	Pred. No. 14		
Matches 75; Conservative	0	Mismatches 70;	Indels 0;	Gaps 0;

0Y 3 CTTATCGGACAGAGAGCGCAGCTTCCTGTGGTCTAACCGCAGCCGAGCACTCCTTA 62
 Db 33 CTTATATGATATCCCCCCCCCTTCTCTCTCGTAGCTGACGCGGACAGCAACCGCTTT 92
 0Y 63 TCGGAACAGAGAGCGCGCTCCATATCAGCGCGCGGTATCTCATGCGCGTACCGGACAG 122
 Db 93 CCTACACGACTGGCACTTCTCTGGAGGAGGAGCAGCGTCCGCGTCCCTTGCACCAAG 152
 0Y 123 AGCGCGCGGTCCCGGCTTATCGCGCC 147
 Db 153 GACAGAGCGTCCCGCTTCCCTTCC 177

Search completed: June 15, 2006, 18:15:44
Job time : 1485.21 secs

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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 15, 2006, 16:32:43 ; Search time 60.6721 Seconds
(without alignments)
5458.628 Million cell updates/sec

Title: US-09-896-888a-1_COPY_351_527

Perfect score: 177

Sequence: 1 gctctatcgtagacagagcgc.....gcccgcaagatcgtgtaaa 177

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

Issued Patents_NA:*

1: /EMC Celerra_SIDS3/prodata/2/ina/1 COMB.seq:*

2: /EMC Celerra_SIDS3/prodata/2/ina/5 COMB.seq:*

3: /EMC Celerra_SIDS3/prodata/2/ina/6 COMB.seq:*

4: /EMC Celerra_SIDS3/prodata/2/ina/6 COMB.seq:*

5: /EMC Celerra_SIDS3/prodata/2/ina/7 COMB.seq:*

6: /EMC Celerra_SIDS3/prodata/2/ina/7 COMB.seq:*

7: /EMC Celerra_SIDS3/prodata/2/ina/H COMB.seq:*

8: /EMC Celerra_SIDS3/prodata/2/ina/H COMB.seq:*

9: /EMC Celerra_SIDS3/prodata/2/ina/H COMB.seq:*

10: /EMC Celerra_SIDS3/prodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	30	16.9	1710	US-09-252-991A-12692
2	29.8	16.8	1311	US-09-902-540-2371
3	29.8	16.8	13579	US-09-902-540-1101
4	28.6	16.2	585	US-09-252-991A-12370
5	28.6	16.2	1443	US-09-252-991A-12097
6	28.6	16.2	1551	US-09-252-991A-12323
7	28.6	16.2	2085	US-09-252-991A-12337
8	28.6	16.2	2091	US-08-899-437-22
9	28.6	16.2	2091	US-09-126-121-22
10	28.6	16.2	2091	US-09-107-979-22
11	28.6	16.2	2502	US-08-899-437-5
12	28.6	16.2	2502	US-09-126-121-5
13	28.6	16.2	2502	US-09-107-979-5
14	28.6	16.2	25048	US-09-902-540-1239
15	28.4	16.0	57320	US-09-949-016-13983
16	28.4	15.9	283	US-09-902-540-7217
17	28.2	15.9	2892	US-09-902-540-674
18	28.2	15.9	126200	US-09-949-016-11824
19	28.2	15.9	126200	US-09-949-016-13183
20	27.8	15.7	601	US-09-949-016-19425
21	27.8	15.7	601	US-09-949-016-49606
22	27.8	15.7	2208	US-09-902-540-7028
23	27.8	15.7	2208	US-09-902-540-7028

24	27.8	15.7	5588	3	US-09-902-540-621	Sequence 621, App
25	27.6	15.6	534	3	US-09-489-039A-2740	Sequence 2740, App
26	27.6	15.6	798	3	US-09-489-039A-2763	Sequence 2763, App
27	27.4	15.5	37838	3	US-09-949-016-12134	Sequence 12134, A
28	27.4	15.5	188504	3	US-09-949-002-711	Sequence 711, App
29	27.4	15.5	200918	3	US-09-949-002-647	Sequence 647, App
30	27.2	15.4	549	3	US-09-902-540-6433	Sequence 6433, App
31	27.2	15.4	978	3	US-09-252-991A-14837	Sequence 14837, A
32	27.2	15.4	999	3	US-09-252-991A-14970	Sequence 14970, A
33	27.2	15.4	1377	3	US-09-902-540-2474	Sequence 2474, App
34	27.2	15.4	1524	3	US-09-489-039A-5551	Sequence 5551, App
35	27.2	15.4	4194	3	US-09-902-540-2099	Sequence 2099, App
36	27.2	15.4	4902	3	US-09-902-540-5635	Sequence 5635, App
37	27.2	15.4	8563	3	US-09-902-540-3318	Sequence 3318, App
38	27.2	15.4	9080	3	US-09-902-540-1963	Sequence 1963, App
39	27.2	15.4	12865	3	US-09-902-540-1048	Sequence 1048, App
40	27.2	15.4	15209	3	US-09-902-540-1110	Sequence 1110, App
41	27.2	15.4	15351	3	US-09-902-540-1154	Sequence 1154, App
42	27.2	15.4	49225	3	US-09-902-540-1269	Sequence 1269, App
43	27	15.3	1182	3	US-09-252-991A-200	Sequence 200, App
44	27	15.3	1230	3	US-10-105-319-1	Sequence 1, App11
45	27	15.3	1230	3	US-10-237-060-2	Sequence 2, App11

ALIGNMENTS

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RESULT 1
US-09-252-991A-12692/c
; Sequence 12692, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: 1999-02-18
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 12692
; LENGTH: 1710
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
; US-09-252-991A-12692

Query Match 16.9%; Score 30; DB 3; Length 1710;
Best Local Similarity 57.4%; Pred. No. 4.2;
Matches 54; Conservative 0; Mismatches 40; Indels 0; Gaps 0;

Qy 81 CCATATCAGCGCGCGCTATCTCATCGCGTACCGGACGAGCGCGCGCTTAA 140
Db 414 CCAAAATAGCGGCTCATCTCTGGGAGATGACGGGGACCTTGGAGGCGATTGCCCC 355
Qy 141 TCGCGCTATTAATACAGCCCGCAACGATCTGCT 174
Db 354 TCGCCCCGTCACTCGTCATCCACCTCGAGCT 321

RESULT 2
US-09-902-540-2371
; Sequence 2371, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
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CURRENT APPLICATION NUMBER: US/09/902,540
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: 60/217,883
PRIOR FILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 16825
SEQ ID NO 2371
LENGTH: 1311
TYPE: DNA
ORGANISM: Myxococcus xanthus
US-09-902-540-2371

Query Match
Best Local Similarity 55.2%; Score 29.8; DB 3; Length 1311;
Pred. No. 4.6;
Matches 58; Conservative 0; Mismatches 47; Indels 0; Gaps 0;

QY 45 GCGGACGCAACTCTTATCGGAACAGACGCGCTCCATATCAAGCGCGGTATCTCA 104
DB 368 GCGGACGCAACTCTTATCGGAACAGACGCGCTCCATATCAAGCGCGGTATCTCA 427
QY 105 TGCGCGTGAACGAGACGAGCGCGCTCCATATCGGCGCTTA 149
DB 428 GGAACGGACATTGACGAGCGCGCGGTCAAGCTTTACCCCA 472

RESULT 3
US-09-902-540-1101/c
Sequence 1101, Application US/09902540
Patent No. 6833447
GENERAL INFORMATION:
APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Wiegand, Roger C.
TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
FILE REFERENCE: 38-10(115849)B
CURRENT APPLICATION NUMBER: US/09/902,540
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: 60/217,883
PRIOR FILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 16825
SEQ ID NO 1101
LENGTH: 13579
TYPE: DNA
ORGANISM: Myxococcus xanthus
US-09-902-540-1101

Query Match
Best Local Similarity 55.2%; Score 29.8; DB 3; Length 13579;
Pred. No. 7.7;
Matches 58; Conservative 0; Mismatches 47; Indels 0; Gaps 0;

QY 45 GCGGACGCAACTCTTATCGGAACAGACGCGCTCCATATCAAGCGCGGTATCTCA 104
DB 1063 GCGGACGCAACTCTTATCGGAACAGACGCGCTCCATATCAAGCGCGGTATCTCA 1004
QY 105 TGCGCGTGAACGAGACGAGCGCGCTCCATATCGGCGCTTA 149
DB 1003 GGAACGGACATTGACGAGCGCGCGGTCAAGCTTTACCCCA 959

RESULT 4
US-09-252-991A-12370/c
Sequence 12370, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 12370
LENGTH: 585
TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-12370

Query Match
Best Local Similarity 53.0%; Score 28.6; DB 3; Length 585;
Pred. No. 9.4;
Matches 61; Conservative 0; Mismatches 54; Indels 0; Gaps 0;

QY 8 CGTACAGACGCGCACTTCTGTGTGCTAATACGAGCGGACGCAACTCTTATCGGA 67
DB 534 CGTACGCTGTGACAGGCGCTGTGTGCTAATACGAGCGGACGCAACTCTTATCGGA 475
QY 68 ACAGAGCGCGCTTCAATATCAAGCGCGCTTATCTATGCGGTGACCGGACAG 122
DB 474 GCTGACGCGCGGCAATATCAAGCGCGCTTATCTATGCGGTGACCGGACAG 420

RESULT 5
US-09-252-991A-12097
Sequence 12097, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 12097
LENGTH: 1443
TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-12097

Query Match
Best Local Similarity 53.0%; Score 28.6; DB 3; Length 1443;
Pred. No. 11;
Matches 61; Conservative 0; Mismatches 54; Indels 0; Gaps 0;

QY 8 CGTACAGACGCGCACTTCTGTGTGCTAATACGAGCGGACGCAACTCTTATCGGA 67
DB 810 CGTACGCTGTGACAGGCGCTGTGTGCTAATACGAGCGGACGCAACTCTTATCGGA 869
QY 68 ACAGAGCGCGCTTCAATATCAAGCGCGCTTATCTATGCGGTGACCGGACAG 122
DB 870 GCTGACGCGCGGCAATATCAAGCGCGCTTATCTATGCGGTGACCGGACAG 924

RESULT 6
US-09-252-991A-12323/c
Sequence 12323, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 12323

LENGTH: 1551
TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-12323

Query Match 16.2%; Score 28.6; DB 3; Length 1551;
Best Local Similarity 53.0%; Pred. No. 12;
Matches 61; Conservative 0; Mismatches 54; Indels 0; Gaps 0;

QY 8 CGTACAGAGCGCCCTCTCTGTTCTTAACCGCAGCCGAGCACTCTTATCGGA 67
DB 715 CGTGCCTGCTGGCAGGGGCTGTGTCGAGCCGATGCCGCTTCGATACCGTGTGCA 656
QY 68 ACAGAGCGCGCCCTCATATCAGCGCGCTTATCTCATGCGCGAGCAGC 122
DB 655 GCTGACCGCCCGCAGATCAAGCCGACGTTAGCTGGGGCAGTGGCGGAAATG 601

RESULT 7

US-09-252-991A-12237
Sequence 12237, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
FILE REFERENCE: 107196, 136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 12237
LENGTH: 2085
TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-12237

Query Match 16.2%; Score 28.6; DB 3; Length 2085;
Best Local Similarity 53.0%; Pred. No. 12;
Matches 61; Conservative 0; Mismatches 54; Indels 0; Gaps 0;

QY 8 CGTACAGAGCGCCCTCTCTGTTCTTAACCGCAGCCGAGCACTCTTATCGGA 67
DB 802 CGTGCCTGCTGGCAGGGGCTGTGTCGAGCCGATGCCGCTTCGATACCGTGTGCA 861
QY 68 ACAGAGCGCGCCCTCATATCAGCGCGCTTATCTCATGCGCGAGCAGC 122
DB 862 GCTGACCGCCCGCAGATCAAGCCGACGTTAGCTGGGGCAGTGGCGGAAATG 916

RESULT 8

US-08-899-437-22
Sequence 22, Application US/08899437
Patent No. 6121415
GENERAL INFORMATION:
APPLICANT: Godowski, Paul J., Mark, Melanie Rose, Zhang, Dong Xiao
TITLE OF INVENTION: ErbB Receptor-Specific Neuregulin Related
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WinPatIn (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/899,437

FILING DATE: 24-Jul-1997

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Conley, Deirdre L.

REGISTRATION NUMBER: 36,487

REFERENCE/DOCKET NUMBER: P1084R1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650/225-2066

TELEFAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 22:

SEQUENCE CHARACTERISTICS:

LENGTH: 2091 base pairs

TYPE: Nucleic Acid

STRANDEDNESS: Single

TOPOLOGY: Linear

FEATURE:

NAME/KEY: Human NR3B2 (hNR3B2)

LOCATION: 1-2091

IDENTIFICATION METHOD:

OTHER INFORMATION:

US-08-899-437-22

Query Match 16.2%; Score 28.6; DB 3; Length 2091;
Best Local Similarity 58.0%; Pred. No. 12;
Matches 69; Conservative 0; Mismatches 49; Indels 1; Gaps 1;

QY 55 ACTCTTATCGGAACAGAGCGCCCTTCATATCAGCGCGCTTATCTCATGCGCGGAC 114
DB 448 ACCGCCAACCGGATTAGACTCCCTGACCAACA-TCAGCGGGCGGCCACTGCTTCCC 506
QY 115 CGAGACAGAGCGCCCGCTCCGCTTATCGCGCTTATTAATACAGCCGCAACGATCG 173
DB 507 CGGACACGGGGTCCCATCCGAGCCGCGCTCCACCAAGACAGCAAGCACTGGG 565

RESULT 9

US-09-126-121-22
Sequence 22, Application US/09126121
Patent No. 6252051
GENERAL INFORMATION:
APPLICANT: Godowski, Paul J., Mark, Melanie Rose, Zhang, Dong Xiao
TITLE OF INVENTION: ErbB Receptor-Specific Neuregulin Related
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/126,121
FILING DATE: 30-Jul-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Conley, Deirdre L.
REGISTRATION NUMBER: 36,487
REFERENCE/DOCKET NUMBER: P1084R1D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-2066
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 2091 base pairs

TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
FEATURE: Human NR3B2 (hNR3B2)
LOCATION: 1-2091
IDENTIFICATION METHOD:
OTHER INFORMATION:
US-09-126-121-22

Query Match 16.2%; Score 28.6; DB 3; Length 2091;
Best Local Similarity 58.0%; Pred. No. 12;
Matches 69; Conservative 0; Mismatches 49; Indels 1; Gaps 1;

QY 55 ACTCCTTATCGGAACGAGCGCCCTTCATATCAGCCGCGCAACGATCTGG 114
DB 448 ACGCCCAACCGGATTACACTCGCTTACCAACCA-TCACGCGGCGCCCTGCTCC 506
QY 115 CGGACAGAGCGCGCCGCTTATCGGCGCTATAATACAGCCGCAACGATCTGG 173
DB 507 CGGGCACCGGGTGCCTATCCGGCGCAAGCCGCTCCACACAGCAGCAACTGCGG 565

RESULT 10
US-09-107-979-22
Sequence 22, Application US/09107979
Patent No. 6994856
GENERAL INFORMATION:
APPLICANT: Godowski, Paul J., Mark, Melanie Rose, Zhang, Dong Xiao
TITLE OF INVENTION: ErbB Receptor-Specific Neuregulin Related
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107, 979
FILING DATE: 30-Jun-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Conley, Deirdre L.
REGISTRATION NUMBER: 36,487
REFERENCE/DOCKET NUMBER: P1084R1-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-2066
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 2091 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
FEATURE:
NAME/KEY: Human NR3B2 (hNR3B2)
LOCATION: 1-2091
IDENTIFICATION METHOD:
OTHER INFORMATION:
US-09-107-979-22

Query Match 16.2%; Score 28.6; DB 4; Length 2091;
Best Local Similarity 58.0%; Pred. No. 12;
Matches 69; Conservative 0; Mismatches 49; Indels 1; Gaps 1;
QY 55 ACTCCTTATCGGAACGAGCGCCCTTCATATCAGCCGCGCTTATCTATCGCGCTGAC 114

DB 448 ACGCCCAACCGGATTACACTCGCTTACCAACCA-TCACGCGGCGCCCTGCTCC 506
QY 115 CGGACAGAGCGCGCCGCTTATCGGCGCTATAATACAGCCGCAACGATCTGG 173
DB 507 CGGGCACCGGGTGCCTATCCGGCGCAAGCCGCTCCACACAGCAGCAACTGCGG 565

RESULT 11
US-08-899-437-5
Sequence 5, Application US/08899437
Patent No. 6121415
GENERAL INFORMATION:
APPLICANT: Godowski, Paul J., Mark, Melanie Rose, Zhang, Dong Xiao
TITLE OF INVENTION: ErbB Receptor-Specific Neuregulin Related
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/899,437
FILING DATE: 24-Jul-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Conley, Deirdre L.
REGISTRATION NUMBER: 36,487
REFERENCE/DOCKET NUMBER: P1084R1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-2066
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 2502 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
FEATURE:
NAME/KEY: Human NR3B1 (hNR3B1)/nucleic acid seq.
LOCATION: 1-2502
IDENTIFICATION METHOD:
OTHER INFORMATION:
US-08-899-437-5

Query Match 16.2%; Score 28.6; DB 3; Length 2502;
Best Local Similarity 58.0%; Pred. No. 13;
Matches 69; Conservative 0; Mismatches 49; Indels 1; Gaps 1;

QY 55 ACTCCTTATCGGAACGAGCGCCCTTCATATCAGCCGCGCTTATCTCATCGGCTGAC 114
DB 591 ACGCCCAACCGGATTACACTCGCTTACCAACCA-TCACGCGGCGCCCTGCTCC 649
QY 115 CGGACAGAGCGCGCCGCTTATCGGCGCTATAATACAGCCGCAACGATCTGG 173
DB 650 CGGGCACCGGGTGCCTATCCGGCGCAAGCCGCTCCACACAGCAGCAACTGCGG 708

RESULT 12
US-09-126-121-5
Sequence 5, Application US/09126121
Patent No. 6252051
GENERAL INFORMATION:
APPLICANT: Godowski, Paul J., Mark, Melanie Rose, Zhang, Dong Xiao
TITLE OF INVENTION: ErbB Receptor-Specific Neuregulin Related

RESULT 15

US-09-949-016-13983/C
; Sequence 13983, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ. ID NOS: 207012
; SOFTWARE: PastSeq for Windows Version 4.0
; SEQ. ID NO 13983
; LENGTH: 57320
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(57320)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-13983

Query Match

16.0%; Score 28.4; DB 3; Length 57320;

Best Local Similarity 49.3%; Pred. No. 31;

Matches 74; Conservative 0; Mismatches 76; Indels 0; Gaps 0;

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DB	2034	GGA	ACCGCATCTTCTCTGACAGCCCGACGAGCCCGCAGCAGCAGCAACCGTC	1975
QY	75	GCG	CTTCATATACAGCCGCGCTTATCTCATGCGCGGTGACCGAGACAGAGCGCCGTC	134
DB	1974	GCG	GTCACTTCGCGGAGCGCGCGCTTGCAACGCTCAGCGACTCCGCCCGCG	1915
QY	135	CGC	TATCGGCGCTTAAATACAGCCGCA	164
DB	1914	GCG	CGGCGGCGACCGAGGAGACGCGCA	1885

Search completed: June 15, 2006, 17:18:11
Job time : 62.6721 secs

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 15, 2006, 17:18:32 ; Search time 598.121 Seconds
(without alignments)
3636.237 Million cell updates/sec

Title: US-09-896-888a-1_COPY_351_527

Perfect score: 177

Sequence: 1 gctctatcgagcagcagcgc.....gccccaacgactctgtraa 177

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications NA Main:*

1: /EMC Celerra_SIDS3/ptodata/2/pubpna/US07_PUBCOMB.seq:*
2: /EMC Celerra_SIDS3/ptodata/2/pubpna/US08_PUBCOMB.seq:*
3: /EMC Celerra_SIDS3/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
4: /EMC Celerra_SIDS3/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
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8: /EMC Celerra_SIDS3/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
9: /EMC Celerra_SIDS3/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
10: /EMC Celerra_SIDS3/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
11: /EMC Celerra_SIDS3/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
12: /EMC Celerra_SIDS3/ptodata/2/pubpna/US10G_PUBCOMB.seq:*
13: /EMC Celerra_SIDS3/ptodata/2/pubpna/US11A_PUBCOMB.seq:*
14: /EMC Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*
15: /EMC Celerra_SIDS3/ptodata/2/pubpna/US11C_PUBCOMB.seq:*
16: /EMC Celerra_SIDS3/ptodata/2/pubpna/US11D_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	177	100.0	462	3	US-09-896-888a-14
2	177	100.0	560	3	US-10-622-088-126
3	177	100.0	564	3	US-09-896-888a-1
4	177	100.0	2773	9	US-10-295-074-60
5	177	100.0	2773	9	US-10-846-911-60
6	177	100.0	2773	9	US-10-939-107-60
7	175.4	99.1	5038	9	US-10-622-088-89
8	41	23.2	147	9	US-10-622-088-127
9	41	23.2	325	9	US-10-622-088-149
10	32.2	18.2	3138	7	US-10-156-761-2538
11	32.2	18.2	9025608	7	US-10-156-761-1
12	32.2	18.1	921	10	US-10-779-543-8561
13	30.8	17.4	1268	13	US-11-097-143-25442
14	30.8	17.4	1342	13	US-11-097-143-38495
15	30.8	17.4	3448	13	US-11-097-143-38494
16	30.8	17.4	3600	13	US-11-097-143-25441
17	30.6	17.3	1404	7	US-10-369-493-45503

18	30.6	17.3	10968	15	US-11-075-185-35	Sequence 35, Appl
19	30.6	17.3	78869	15	US-11-075-185-1	Sequence 1, Appl
20	30.2	17.1	1116	8	US-10-437-863-42126	Sequence 42126, A
21	30.2	17.1	2472	8	US-10-437-863-55473	Sequence 55473, A
22	30	16.9	657	8	US-10-259-194A-563	Sequence 563, App
23	30	16.9	6107	8	US-10-221-613-303	Sequence 303, App
24	29.8	16.8	1370	8	US-10-275-311A-10	Sequence 10, Appl
25	29.8	16.8	1769	13	US-11-097-143-26108	Sequence 26108, A
26	29.8	16.8	3915	13	US-11-097-143-26107	Sequence 26107, A
27	29.6	16.7	300	10	US-10-779-543-7296	Sequence 7296, Ap
28	29.6	16.7	1798	9	US-10-739-930-4094	Sequence 4094, Ap
29	29.6	16.7	3498	8	US-10-437-863-72869	Sequence 72869, A
30	29.4	16.6	1923	8	US-10-437-863-50761	Sequence 50761, A
31	29.4	16.6	5118	8	US-10-437-863-35667	Sequence 35667, A
32	29.2	16.5	1593	7	US-10-369-493-44133	Sequence 44133, A
33	28.8	16.3	646	4	US-09-925-065A-711960	Sequence 711960, A
34	28.8	16.3	646	5	US-09-925-065A-711960	Sequence 65984, A
35	28.6	16.2	823	7	US-10-029-386-22976	Sequence 22976, A
36	28.6	16.2	915	10	US-10-450-763-6584	Sequence 6584, Ap
37	28.6	16.2	1425	3	US-09-815-242-4072	Sequence 4072, Ap
38	28.6	16.2	1425	8	US-10-482-122A-7326	Sequence 7326, Ap
39	28.6	16.2	1434	7	US-10-369-493-32534	Sequence 32534, A
40	28.6	16.2	2091	3	US-09-817-647-22	Sequence 22, Appl
41	28.6	16.2	2091	3	US-09-817-647-22	Sequence 22, Appl
42	28.6	16.2	2091	3	US-09-817-647-22	Sequence 22, Appl
43	28.6	16.2	2091	6	US-10-136-573A-22	Sequence 22, Appl
44	28.6	16.2	2091	6	US-10-215-862-22	Sequence 22, Appl
45	28.6	16.2	2091	10	US-10-944-116-22	Sequence 22, Appl

ALIGNMENTS

RESULT 1
US-09-896-888a-14
; Sequence 14, Application US/09896888A
; Patent No. US20020116723A1
; GENERAL INFORMATION:
; APPLICANT: The University of British Columbia
; TITLE OF INVENTION: Insect Expression Vectors
; FILE REFERENCE: 80021-44
; CURRENT APPLICATION NUMBER: US/09/896, 888A
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US/09/048, 911
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/049, 946
; PRIOR FILING DATE: 1997-03-27
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 462
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Promoter
; OTHER INFORMATION: Sequence of the Opmpv 1ez gene
US-09-896-888a-14
Query Match 100.0%; Score 177; DB 3; Length 462;
Best Local Similarity 100.0%; Pred. No. 2,9e-54;
Matches 177; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTTTATCGTACAGACGCGCTTCTGTGTGCTAACCGACGCGCACTCCT 60
DB 250 GTTTATCGTACAGACGCGCTTCTGTGTGCTAACCGACGCGCACTCCT 309
QY 61 TATCGAAGACGACGCGCTTCATATCACCGGCGCTTATCATCGCGGTACCGAGAA 120
DB 310 TATCGAAGACGACGCGCTTCATATCACCGGCGCTTATCATCGCGGTACCGAGAA 369
QY 121 CGAGGCGCGCTTCCGCTTATCGCGCTTAAATACAGCCGCAAGATCTGTATA 177
DB 370 CGAGGCGCGCTTCCGCTTATCGCGCTTAAATACAGCCGCAAGATCTGTATA 426

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RESULT 2
US-10-622-088-126
; Sequence 126, Application US/10622088
; Publication No. US20040219516A1
; GENERAL INFORMATION:
; APPLICANT: Bennett, Robert P.
; APPLICANT: Welch, Peter J.
; APPLICANT: Harwood, Steven
; APPLICANT: Madden, Knut
; APPLICANT: Frimpong, Kenneth
; APPLICANT: Franke, Kenneth E.
; TITLE OF INVENTION: Viral Vectors Containing Recombination Sites
; FILE REFERENCE: 0942.545007
; CURRENT APPLICATION NUMBER: US/10/622,088
; PRIOR FILING DATE: 2003-07-18
; PRIOR APPLICATION NUMBER: PCT/US03/22437
; PRIOR FILING DATE: 2003-07-18
; PRIOR APPLICATION NUMBER: US 60/396,335
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: US 60/398,617
; PRIOR FILING DATE: 2002-07-26
; PRIOR APPLICATION NUMBER: US 60/427,231
; PRIOR FILING DATE: 2002-11-19
; PRIOR APPLICATION NUMBER: US 60/456,486
; PRIOR FILING DATE: 2003-03-24
; PRIOR APPLICATION NUMBER: US 60/474,940
; PRIOR FILING DATE: 2003-06-03
; NUMBER OF SEQ ID NOS: 165
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 126
; LENGTH: 560
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: OpIez promoter sequence
US-10-622-088-126

Query Match      100.0%; Score 177; DB 9; Length 560;
Best Local Similarity 100.0%; Pred. No. 3e-54;
Matches 177; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  GTCTTATCGTAGACGAGCGCAGCTTCTGTGTGCTTACCGGACCGGACGAACTCCT 60
DB      355  GTCTTATCGTAGACGAGCGCAGCTTCTGTGTGCTTACCGGACCGGACGAACTCCT 414
QY      61  TATCGAACAAGACGCGCCTTCATATACGCGCGCTTATCTCATYGGCGGTGACCGGACA 120
DB      415  TATCGAACAAGACGCGCCTTCATATACGCGCGCTTATCTCATYGGCGGTGACCGGACA 474
QY      121  CGAGGCGCCCGTCCCGCTTATCGGCTTAAATACGCCCCGCAAGCATCTGGTAAA 177
DB      475  CGAGGCGCCCGTCCCGCTTATCGGCTTAAATACGCCCCGCAAGCATCTGGTAAA 531

RESULT 3
US-09-896-888a-1
; Sequence 1, Application US/09896888A
; Patent No. US20020116723A1
; GENERAL INFORMATION:
; APPLICANT: The University of British Columbia
; TITLE OF INVENTION: Insect Expression Vectors
; FILE REFERENCE: 80021-44
; CURRENT APPLICATION NUMBER: US/09/896,888A
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US/09/048,911
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/049,946
; PRIOR FILING DATE: 1997-03-27
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
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; LENGTH: 564
; TYPE: DNA
; ORGANISM: Orygia pseudotsugata
US-09-896-888a-1

Query Match      100.0%; Score 177; DB 3; Length 564;
Best Local Similarity 100.0%; Pred. No. 3e-54;
Matches 177; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  GTCTTATCGTAGACGAGCGCAGCTTCTGTGTGCTTACCGGACCGGACGAACTCCT 60
DB      351  GTCTTATCGTAGACGAGCGCAGCTTCTGTGTGCTTACCGGACCGGACGAACTCCT 410
QY      61  TATCGAACAAGACGCGCCTTCATACGCGCGCTTATCTCATGCGGTGACCGGACA 120
DB      411  TATCGAACAAGACGCGCCTTCATACGCGCGCTTATCTCATGCGGTGACCGGACA 470
QY      121  CGAGGCGCCCGTCCCGCTTATCGGCTTAAATACGCCCCGCAAGCATCTGGTAAA 177
DB      471  CGAGGCGCCCGTCCCGCTTATCGGCTTAAATACGCCCCGCAAGCATCTGGTAAA 527

RESULT 4
US-10-295-074-60
; Sequence 60, Application US/10295074
; Publication No. US20030185845A1
; GENERAL INFORMATION:
; APPLICANT: Pharmexa A/S
; TITLE OF INVENTION: NOVEL IMMUNOGENIC MIMETICS OF MULTIMER PROTEINS
; FILE REFERENCE: P1013DK00
; CURRENT APPLICATION NUMBER: US/10/295,074
; PRIOR FILING DATE: 2002-11-15
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 60
; LENGTH: 2773
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: p2Zop2f expression vector for insect cells
; FEATURE:
; NAME/KEY: misc_recomb
; LOCATION: (561)..(566)
; OTHER INFORMATION: HindIII site
; FEATURE:
; NAME/KEY: misc_recomb
; LOCATION: (573)..(578)
; OTHER INFORMATION: AvalI site
; FEATURE:
; NAME/KEY: misc_recomb
; LOCATION: (586)..(591)
; OTHER INFORMATION: EcoRI site
; FEATURE:
; NAME/KEY: misc_recomb
; LOCATION: (593)..(598)
; OTHER INFORMATION: BamHI site
; FEATURE:
; NAME/KEY: misc_recomb
; LOCATION: (629)..(634)
; OTHER INFORMATION: ClaI site
; FEATURE:
; NAME/KEY: misc_recomb
; LOCATION: (1156)..(1161)
; OTHER INFORMATION: ApaLI site
; FEATURE:
; NAME/KEY: misc_recomb
; LOCATION: (2128)..(2133)
; OTHER INFORMATION: PstI site
; FEATURE:
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NAME/KEY: misc_recomb
LOCATION: (2204)..(2209)
OTHER INFORMATION: NcoI site
FEATURE:
NAME/KEY: misc_recomb
LOCATION: (2284)..(2289)
OTHER INFORMATION: AatI site
FEATURE:
NAME/KEY: misc_recomb
LOCATION: (2294)..(2299)
OTHER INFORMATION: AatI, SmaI, and XmaI site
FEATURE:
NAME/KEY: misc_recomb
LOCATION: (2551)..(2556)
OTHER INFORMATION: AatI site
US-10-295-074-60

Query Match 100.0%; Score 177; DB 7; Length 2773;
Best Local Similarity 100.0%; Pred. No. 3.8e-54;
Matches 177; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTCTTATCGTGAAGAGAGCGGCTTCTGTGTGTTGTTAACCAGCGCGGAGCACTCT 60
DB 355 GTCTTATCGTGAAGAGAGCGGCTTCTGTGTGTTGTTAACCAGCGCGGAGCACTCT 414
QY 61 TATCGGAACAGAGAGCGGCTTCTGTGTGTTGTTAACCAGCGCGGAGCACTCT 120
DB 415 TATCGGAACAGAGAGCGGCTTCTGTGTGTTGTTAACCAGCGCGGAGCACTCT 474
QY 121 CGAGGGCCCGGCTTCTGTGTGTTGTTAACCAGCGCGGAGCACTCT 177
DB 475 CGAGGGCCCGGCTTCTGTGTGTTGTTAACCAGCGCGGAGCACTCT 531

RESULT 5
US-10-846-911-60
Sequence 60. Application US/10846911
Publication No. US20040258660A1
GENERAL INFORMATION:
APPLICANT: KLYSNER, Steen
APPLICANT: NIELSEN, Finn Stausholm
APPLICANT: BRATT, Tomas
APPLICANT: VOLDORF, Bjorn
TITLE OF INVENTION: NOVEL IMMUNOGENIC MIMETICS OF MULTIMER PROTEINS
FILE REFERENCE: 674542-2018
CURRENT APPLICATION NUMBER: US/10/846, 911
CURRENT FILING DATE: 2004-05-14
PRIOR APPLICATION NUMBER: PCT/DK02/00764
PRIOR FILING DATE: 2002-11-15
PRIOR APPLICATION NUMBER: 60/331,575
PRIOR FILING DATE: 2001-11-16
PRIOR APPLICATION NUMBER: PA 2001 01702
NUMBER OF SEQ ID NOS: 60
SOFTWARE: PatentIn version 3.1
SEQ ID NO 60
LENGTH: 2773
TYPE: DNA
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: p2ZOP2F expression vector for insect cells
FEATURE:
NAME/KEY: misc_recomb
LOCATION: (561)..(566)
OTHER INFORMATION: HindIII site
FEATURE:
NAME/KEY: misc_recomb
LOCATION: (573)..(578)
OTHER INFORMATION: AatI site
FEATURE:
NAME/KEY: misc_recomb
LOCATION: (586)..(591)

OTHER INFORMATION: EcoRI site
FEATURE:
NAME/KEY: misc_recomb
LOCATION: (593)..(598)
OTHER INFORMATION: BamHI site
FEATURE:
NAME/KEY: misc_recomb
LOCATION: (625)..(630)
OTHER INFORMATION: ClaI site
FEATURE:
NAME/KEY: misc_recomb
LOCATION: (629)..(634)
OTHER INFORMATION: ClaI site
FEATURE:
NAME/KEY: misc_recomb
LOCATION: (1156)..(1161)
OTHER INFORMATION: AatI site
FEATURE:
NAME/KEY: misc_recomb
LOCATION: (2128)..(2133)
OTHER INFORMATION: PstI site
FEATURE:
NAME/KEY: misc_recomb
LOCATION: (2204)..(2209)
OTHER INFORMATION: NcoI site
FEATURE:
NAME/KEY: misc_recomb
LOCATION: (2284)..(2289)
OTHER INFORMATION: AatI site
FEATURE:
NAME/KEY: misc_recomb
LOCATION: (2294)..(2299)
OTHER INFORMATION: AatI, SmaI, and XmaI site
FEATURE:
NAME/KEY: misc_recomb
LOCATION: (2551)..(2556)
OTHER INFORMATION: AatI site
US-10-846-911-60

Query Match 100.0%; Score 177; DB 9; Length 2773;
Best Local Similarity 100.0%; Pred. No. 3.8e-54;
Matches 177; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTCTTATCGTGAAGAGAGCGGCTTCTGTGTGTTGTTAACCAGCGCGGAGCACTCT 60
DB 355 GTCTTATCGTGAAGAGAGCGGCTTCTGTGTGTTGTTAACCAGCGCGGAGCACTCT 414
QY 61 TATCGGAACAGAGAGCGGCTTCTGTGTGTTGTTAACCAGCGCGGAGCACTCT 120
DB 415 TATCGGAACAGAGAGCGGCTTCTGTGTGTTGTTAACCAGCGCGGAGCACTCT 474
QY 121 CGAGGGCCCGGCTTCTGTGTGTTGTTAACCAGCGCGGAGCACTCT 177
DB 475 CGAGGGCCCGGCTTCTGTGTGTTGTTAACCAGCGCGGAGCACTCT 531

RESULT 6
US-10-939-107-60
Sequence 60. Application US/10939107
Publication No. US20050180947A1
GENERAL INFORMATION:
APPLICANT: Pedersen, Hans Rudolf
APPLICANT: Ederl, Bjarte
APPLICANT: Pedersen, Louise Henriette
APPLICANT: Rasmussen, Peter Birk
TITLE OF INVENTION: Novel Application of Vaccination Against TNF-alpha
FILE REFERENCE: 674542-2020
CURRENT APPLICATION NUMBER: US/10/939,107
CURRENT FILING DATE: 2004-09-10
PRIOR APPLICATION NUMBER: PCT/DK03/00147
PRIOR FILING DATE: 2003-03-11
PRIOR APPLICATION NUMBER: 60/363,128
PRIOR FILING DATE: 2002-03-11

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; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 60
; LENGTH: 2773
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: p2ZOp2F expression vector for insect cells
; FEATURE:
; NAME/KEY: misc_recomb
; LOCATION: (561)..(566)
; OTHER INFORMATION: HindIII site
; FEATURE:
; NAME/KEY: misc_recomb
; LOCATION: (573)..(578)
; OTHER INFORMATION: AatI site
; FEATURE:
; NAME/KEY: misc_recomb
; LOCATION: (586)..(591)
; OTHER INFORMATION: EcoRI site
; FEATURE:
; NAME/KEY: misc_recomb
; LOCATION: (593)..(598)
; OTHER INFORMATION: BamHI site
; FEATURE:
; NAME/KEY: misc_recomb
; LOCATION: (625)..(630)
; OTHER INFORMATION: ClaI site
; FEATURE:
; NAME/KEY: misc_recomb
; LOCATION: (629)..(634)
; OTHER INFORMATION: ClaI site
; FEATURE:
; NAME/KEY: misc_recomb
; LOCATION: (1156)..(1161)
; OTHER INFORMATION: ApaLI site
; FEATURE:
; NAME/KEY: misc_recomb
; LOCATION: (2128)..(2133)
; OTHER INFORMATION: PstI site
; FEATURE:
; NAME/KEY: misc_recomb
; LOCATION: (2204)..(2209)
; OTHER INFORMATION: NcoI site
; FEATURE:
; NAME/KEY: misc_recomb
; LOCATION: (2284)..(2289)
; OTHER INFORMATION: AatI site
; FEATURE:
; NAME/KEY: misc_recomb
; LOCATION: (2294)..(2299)
; OTHER INFORMATION: AatI, SmaI, and XbaI site
; NAME/KEY: misc_recomb
; LOCATION: (2551)..(2556)
; OTHER INFORMATION: ApaLI site
US-10-939-107-60

Query Match      100.0%; Score 177; DB 10; Length 2773;
Best Local Similarity 100.0%; Pred. No. 3,8e-54;
Matches 177; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  GTCCTATCGTGAAGAGCGAGCTTCCTGTGTTGCTTAACCGGAGCGGAGCACTCCT 60
DB      355 GTCCTATCGTGAAGAGCGAGCTTCCTGTGTTGCTTAACCGGAGCGGAGCACTCCT 414
QY      61  TATCGAAGAGAGCGGCGCTTCATATCAGCGCGCGTATCTCATGCGCGTGAACGGACA 120
DB      415 TATCGAAGAGAGCGGCGCTTCATATCAGCGCGCGTATCTCATGCGCGTGAACGGACA 474
QY      121 CGAGGCGCGCGTCCCGCTTATCGCGCGCTTAATAATACAGCCCGCAAGATCTGTAAA 177
DB      475 CGAGGCGCGCGTCCCGCTTATCGCGCGCTTAATAATACAGCCCGCAAGATCTGTAAA 531
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RESULT 7
US-10-622-088-89
; Sequence 89, Application US/10622088
; Publication No. US20040219516A1
; GENERAL INFORMATION:
; APPLICANT: Bennett, Robert P.
; APPLICANT: Welch, Peter J.
; APPLICANT: Harwood, Steven
; APPLICANT: Madden, Knut
; APPLICANT: Frimpong, Kenneth
; APPLICANT: Franke, Kenneth E.
; TITLE OF INVENTION: Viral Vectors Containing Recombination Sites
; FILE REFERENCE: 0942,5450007
; CURRENT APPLICATION NUMBER: US/10/622,088
; CURRENT FILING DATE: 2003-07-18
; PRIOR APPLICATION NUMBER: PCT/US03/22437
; PRIOR FILING DATE: 2003-07-18
; PRIOR APPLICATION NUMBER: US 60/396,335
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: US 60/398,617
; PRIOR FILING DATE: 2002-07-26
; PRIOR APPLICATION NUMBER: US 60/427,231
; PRIOR FILING DATE: 2002-11-19
; PRIOR APPLICATION NUMBER: US 60/456,496
; PRIOR FILING DATE: 2003-03-24
; PRIOR APPLICATION NUMBER: US 60/474,940
; PRIOR FILING DATE: 2003-06-03
; NUMBER OF SEQ ID NOS: 165
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 89
; LENGTH: 5038
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PIB/V5-His-DEST
US-10-622-088-89

Query Match      99.1%; Score 175.4; DB 9; Length 5038;
Best Local Similarity 99.4%; Pred. No. 1.6e-53;
Matches 176; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1  GTCCTATCGTGAAGAGCGAGCTTCCTGTGTTGCTTAACCGGAGCGGAGCACTCCT 60
DB      351 GTCCTATCGTGAAGAGCGAGCTTCCTGTGTTGCTTAACCGGAGCGGAGCACTCCT 410
QY      61  TATCGAAGAGAGCGGCGCTTCATATCAGCGCGCGTATCTCATGCGCGTGAACGGACA 120
DB      411 TATCGAAGAGAGCGGCGCTTCATATCAGCGCGCGTATCTCATGCGCGTGAACGGACA 470
QY      121 CGAGGCGCGCGTCCCGCTTATCGCGCGCTTAATAATACAGCCCGCAAGATCTGTAAA 177
DB      471 CGAGGCGCGCGTCCCGCTTATCGCGCGCTTAATAATACAGCCCGCAAGATCTGTAAA 527

RESULT 8
US-10-622-088-127
; Sequence 127, Application US/10622088
; Publication No. US20040219516A1
; GENERAL INFORMATION:
; APPLICANT: Bennett, Robert P.
; APPLICANT: Welch, Peter J.
; APPLICANT: Harwood, Steven
; APPLICANT: Madden, Knut
; APPLICANT: Frimpong, Kenneth
; APPLICANT: Franke, Kenneth E.
; TITLE OF INVENTION: Viral Vectors Containing Recombination Sites
; FILE REFERENCE: 0942,5450007
; CURRENT APPLICATION NUMBER: US/10/622,088
; CURRENT FILING DATE: 2003-07-18
; PRIOR APPLICATION NUMBER: PCT/US03/22437
; PRIOR FILING DATE: 2003-07-18
```

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; PRIOR APPLICATION NUMBER: US 60/396,335
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: US 60/398,617
; PRIOR FILING DATE: 2002-07-26
; PRIOR APPLICATION NUMBER: US 60/427,231
; PRIOR FILING DATE: 2002-11-19
; PRIOR APPLICATION NUMBER: US 60/456,496
; PRIOR FILING DATE: 2003-03-24
; PRIOR APPLICATION NUMBER: US 60/474,940
; PRIOR FILING DATE: 2003-06-03
; NUMBER OF SEQ ID NOS: 165
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 127
; LENGTH: 147
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Recombination region of pIB/V5-His-DEST
; NAME/KEY: misc feature
; LOCATION: (141)..(148)
; OTHER INFORMATION: n may be any nucleotide
US-10-622-088-127
```

```

Query Match      23.2%; Score 41; DB 9; Length 147;
Best Local Similarity 100.0%; Pred. No. 0.00016;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```

QY      137 CTTATCGCGCCTTAATAATACAGCCCGACAGATCTGTAA 177
Db      1 CTTATCGCGCCTTAATAATACAGCCCGACAGATCTGTAA 41
```

```

RESULT 9
US-10-622-088-149
; Sequence 149, Application US/10622088
; Publication No. US20040219516A1
; GENERAL INFORMATION:
; APPLICANT: Bennett, Robert P.
; APPLICANT: Welch, Peter J.
; APPLICANT: Harwood, Steven
; APPLICANT: Madden, Knut
; APPLICANT: Frimpong, Kenneth
; APPLICANT: Franke, Kenneth E.
; TITLE OR INVENTION: Viral Vectors Containing Recombination Sites
; FILE REFERENCE: 0942.545007
; CURRENT APPLICATION NUMBER: US/10/622,088
; CURRENT FILING DATE: 2003-07-18
; PRIOR APPLICATION NUMBER: PCT/US03/22437
; PRIOR FILING DATE: 2003-07-18
; PRIOR APPLICATION NUMBER: US 60/396,335
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: US 60/398,617
; PRIOR FILING DATE: 2002-07-26
; PRIOR APPLICATION NUMBER: US 60/427,231
; PRIOR FILING DATE: 2002-11-19
; PRIOR APPLICATION NUMBER: US 60/456,496
; PRIOR FILING DATE: 2003-03-24
; PRIOR APPLICATION NUMBER: US 60/474,940
; PRIOR FILING DATE: 2003-06-03
; NUMBER OF SEQ ID NOS: 165
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 149
; LENGTH: 325
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Recombination region of pIB/V5 His DEST
; NAME/KEY: misc feature
; LOCATION: (141)..(142)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
```

```

; NAME/KEY: CDS
; LOCATION: (145)..(276)
US-10-622-088-149
```

```

Query Match      23.2%; Score 41; DB 9; Length 325;
Best Local Similarity 100.0%; Pred. No. 0.00018;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```

QY      137 CTTATCGCGCCTTAATAATACAGCCCGACAGATCTGTAA 177
Db      1 CTTATCGCGCCTTAATAATACAGCCCGACAGATCTGTAA 41
```

```

RESULT 10
US-10-156-761-2538/C
; Sequence 2538, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OR INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 2538
; LENGTH: 3138
; TYPE: DNA
; ORGANISM: Streptomyces avermitilis
; NAME/KEY: CDS
; LOCATION: (1)..(3138)
US-10-156-761-2538
```

```

Query Match      18.2%; Score 32.2; DB 7; Length 3138;
Best Local Similarity 61.2%; Pred. No. 0.44;
Matches 52; Conservative 0; Mismatches 33; Indels 0; Gaps 0;
```

```

QY      58 CTTATCGAAGAGAGCGCCTCCATATCAGCGCGGCTTATCTGAGCGGTGACCGG 117
Db      2575 CTTCCACCGAAGCGGAGCGCTCCCTTATGATGATGAGTTGAGTCTCTGCACCGACCGG 2516
QY      118 ACAAGAGCGCGCGCTCCGCTTATC 142
Db      2515 CTTGAGGCGCTCGTCCAGGTCTC 2491
```

```

RESULT 11
US-10-156-761-1
; Sequence 1, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OR INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
```

```

; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 1
; LENGTH: 9025608
; TYPE: DNA
; ORGANISM: Streptomyces avermitilis
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (418715)
; OTHER INFORMATION: a, t, c, g, other or unknown
US-10-156-761-1

Query Match      18.2%; Score 32.2; DB 7; Length 9025608;
Best Local Similarity 61.2%; Pred. No. 1.6;
Matches 52; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

QY      58 CCTATCGAAGAGCGCGCTTCATATCAGCGCGGTTATCTCATGGCGGTGACCGG 117
DB      3129487 CCTCCACCGAACCGAGCGCGCTCCCTTGATGATGAGTTGAGTTCTGACACGACCGG 3129546
QY      118 ACAGAGCGCGCGCTCCCGCTTATC 142
DB      3129547 CCTTGAGGCGCTGCTCCAGGTTCTC 3129571

RESULT 12
US-10-779-543-8561/C
; Sequence 8561, Application US/10779543
; Publication No. US20050227917A1
; GENERAL INFORMATION:
; APPLICANT: Williams et al
; TITLE OF INVENTION: GENE PRODUCTS DIFFERENTIALLY EXPRESSED
; FILE REFERENCE: 2300-21302
; CURRENT APPLICATION NUMBER: US/10/779,543
; PRIOR FILING DATE: 2004-02-12
; PRIOR APPLICATION NUMBER: 10/076,555
; PRIOR FILING DATE: 2002-02-15
; PRIOR APPLICATION NUMBER: 09/217,471
; PRIOR FILING DATE: 1998-12-21
; PRIOR APPLICATION NUMBER: 60/068,755
; PRIOR FILING DATE: 1997-12-23
; PRIOR APPLICATION NUMBER: 60/080,664
; PRIOR FILING DATE: 1998-04-03
; PRIOR APPLICATION NUMBER: 60/105,234
; PRIOR FILING DATE: 1998-10-21
; PRIOR APPLICATION NUMBER: 09/297,648
; PRIOR FILING DATE: 2000-04-10
; PRIOR APPLICATION NUMBER: PCT/US99/01619
; PRIOR FILING DATE: 1999-01-28
; PRIOR APPLICATION NUMBER: 60/072,910
; PRIOR FILING DATE: 1998-01-28
; PRIOR APPLICATION NUMBER: 60/075,954
; PRIOR FILING DATE: 1998-02-24
; PRIOR APPLICATION NUMBER: 60/080,114
; PRIOR FILING DATE: 1998-03-31
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 23767
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8561
; LENGTH: 921
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: 4, 6, 29, 88, 91, 146, 218, 378, 413, 482, 485, 500, 508,
; LOCATION: 531, 573, 585, 623, 637, 642, 651, 662, 697, 704, 724,
; LOCATION: 731, 778, 835, 837, 839, 842, 852, 868, 882, 884, 885, 891,
; LOCATION: 892, 899, 901
; OTHER INFORMATION: n = A,T,C or G
US-10-779-543-8561
```

```

Query Match      18.1%; Score 32; DB 10; Length 921;
Best Local Similarity 51.5%; Pred. No. 0.43;
Matches 68; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

QY      16 GAGCCAGCTTCTGTGTGTTGCTAACCGGAGCGGAGCAACTCTTATCGAAGACAGG 75
DB      157 GCGAGCTGGCGNCCAGAGTGAGTGTCTCCACGCGGATCTCCGCGCTGCGGGAT 98
QY      76 CGCTCCATATCAGCGCGCGGTTATCTCATGCGCGGTGACCGGACGAGCGCGCTCC 135
DB      97 GGGGTGTAANCCACCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 38
QY      136 GCTTATCGGCGC 147
DB      37 TAAATCGAGCC 26

RESULT 13
US-11-097-143-25442
; Sequence 25442, Application US/11097143
; Publication No. US20050208558A1
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
; APPLICANT: et al.
; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
; FILE REFERENCE: CL000728
; CURRENT APPLICATION NUMBER: US/11/097,143
; PRIOR FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: 60/157,832
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: 60/160,191
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/161,932
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: 60/164,769
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/173,383
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/175,693
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 60/184,831
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/191,637
; PRIOR FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 43008
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 25442
; LENGTH: 1268
; TYPE: DNA
; ORGANISM: DROSOPHILA
US-11-097-143-25442

Query Match      17.4%; Score 30.8; DB 13; Length 1268;
Best Local Similarity 55.7%; Pred. No. 1.2;
Matches 59; Conservative 0; Mismatches 47; Indels 0; Gaps 0;

QY      17 AGCGAGCTTCTGTGTGTTGCTAACCGGAGCGGAGCAACTCTTATCGAAGACAGCG 76
DB      657 ACAAGAGCTTCCGGTGAAGTGCCCAAGCGGAGGCTTGTGCTCTGCGCGCTCGGTGCG 716
QY      77 GCCTCATATCAGCGCGCGGTTATCTCATGCGCGGTGACCGGACGAGCAG 122
DB      717 GTTGGACATTTGGCCATACAAATCTCAAGTCCAGAAAGTACAAAG 762

RESULT 14
US-11-097-143-38495
; Sequence 38495, Application US/11097143
; Publication No. US20050208558A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Venter, J. Craig
; APPLICANT: et al.
; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
; FILE REFERENCE: DROSOPHILA GENES.
; FILE REFERENCE: CL000728
; CURRENT APPLICATION NUMBER: US/11/097,143
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: 60/157,832
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: 60/160,191
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/161,932
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: 60/164,769
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/173,383
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/175,693
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 60/184,831
; PRIOR FILING DATE: 2000-02-24
; NUMBER OF SEQ ID NOS: 43008
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 38495
; LENGTH: 1342
; TYPE: DNA
; ORGANISM: DROSOPHILA
US-11-097-143-38495
```

```
Query Match 17.4%; Score 30.8; DB 13; Length 1342;
Best Local Similarity 55.7%; Pred. No. 1.2;
Matches 59; Conservative 0; Mismatches 47; Indels 0; Gaps 0;
```

```
Qy 17 ACCGCACTTCTGTGTGCTAACCGACGCGGACGCACTCTTATCGGAACGAGCG 76
Db 731 ACAACAGCTTCCGATGAGGTGCTCCACAGCGGGTCTTATGCTTGGCGGCTCGGTGGC 790
Qy 77 GCCTCATATCAGCGCGGCTTATCTCATGCGCGGTGACCGGACAG 122
Db 791 GTTGGCACTTGGCCATACCAATCTCAAGTCCAGAAAGTACAG 836
```

```
RESULT 15
US-11-097-143-38494/c
; Sequence 38494, Application US/11097143
; Publication No. US20050208558A1
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
; APPLICANT: et al.
; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
; FILE REFERENCE: DROSOPHILA GENES.
; FILE REFERENCE: CL000728
; CURRENT APPLICATION NUMBER: US/11/097,143
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: 60/157,832
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: 60/160,191
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/161,932
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: 60/164,769
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/173,383
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/175,693
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 60/184,831
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/191,637
```

```
; PRIOR FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 43008
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 38494
; LENGTH: 3448
; TYPE: DNA
; ORGANISM: DROSOPHILA
US-11-097-143-38494
```

```
Query Match 17.4%; Score 30.8; DB 13; Length 3448;
Best Local Similarity 55.7%; Pred. No. 1.5;
Matches 59; Conservative 0; Mismatches 47; Indels 0; Gaps 0;
```

```
Qy 17 ACCGCACTTCTGTGTGCTAACCGACGCGGACGCACTCTTATCGGAACGAGCG 76
Db 1667 ACAACAGCTTCCGATGAGGTGCTCCACAGCGGGTCTTATGCTTGGCGGCTCGGTGGC 1608
Qy 77 GCCTCATATCAGCGCGGCTTATCTCATGCGCGGTGACCGGACAG 122
Db 1607 GTTGGCACTTGGCCATACCAATCTCAAGTCCAGAAAGTACAG 1562
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OM nucleic - nucleic search, using sw model

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Title: US-09-896-888a-1_COPY_351_527

Perfect score: 177
Sequence: 1 gcttctatcgtagacagcgc.....gccgcgaacgctctgtraa 177

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 290227 seqs, 117694381 residues

Total number of hits satisfying chosen parameters: 580454

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Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: /EMC_Celerra_SIDS3/prodata/1/pubpna/US06_NEW_PUB.seq:*
3: /EMC_Celerra_SIDS3/prodata/1/pubpna/US07_NEW_PUB.seq:*
4: /EMC_Celerra_SIDS3/prodata/1/pubpna/US08_NEW_PUB.seq:*
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7: /EMC_Celerra_SIDS3/prodata/1/pubpna/US11_NEW_PUB.seq:*
8: /EMC_Celerra_SIDS3/prodata/1/pubpna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	30.2	17.1	1137	6	US-10-449-902-2563 Sequence 2563, Ap
C 2	30.2	17.1	1128	6	US-10-449-902-19810 Sequence 19810, A
C 3	30.2	17.1	2019	6	US-10-449-902-22046 Sequence 22046, A
C 4	30.2	17.1	2127	6	US-10-449-902-9697 Sequence 9697, Ap
C 5	30	16.9	1114	6	US-10-953-349-32119 Sequence 32119, A
C 6	30	16.9	3107	6	US-10-517-441-401 Sequence 401, App
C 7	30	16.9	3501	6	US-10-517-441-499 Sequence 499, App
C 8	29.6	16.7	2214	6	US-10-449-902-25649 Sequence 25649, A
C 9	29.6	16.7	2586	6	US-10-449-902-24630 Sequence 24630, A
C 10	29.6	16.7	2618	6	US-10-449-902-16689 Sequence 16689, A
C 11	27.6	15.6	788	6	US-10-449-902-14247 Sequence 14247, A
C 12	27.2	15.4	1687	6	US-10-449-902-25610 Sequence 25610, A
C 13	27.2	15.4	2150	6	US-10-449-902-12192 Sequence 12192, A
C 14	26.8	15.1	1710	7	US-11-217-529-1986 Sequence 1986, Ap
C 15	26.8	15.1	1774	6	US-10-449-902-16716 Sequence 16716, A
C 16	26.8	15.1	2816	7	US-11-293-697-831 Sequence 831, App
C 17	26.8	15.1	2911	7	US-11-293-697-1360 Sequence 1360, App
C 18	26.8	15.1	3020	6	US-10-505-928-320 Sequence 320, App
C 19	26.6	15.0	2791	6	US-10-449-902-17961 Sequence 17961, A
C 20	26.4	14.9	974	6	US-10-449-902-1273 Sequence 1273, Ap
C 21	26.4	14.9	1092	7	US-11-217-529-77591 Sequence 77591, A
C 22	26.4	14.9	1848	6	US-10-449-902-376 Sequence 376, App
C 23	26.4	14.9	1848	6	US-10-449-902-8998 Sequence 8998, App
C 24	26.4	14.9	3169	6	US-10-449-902-12991 Sequence 12991, A
C 25	26	14.7	2768	6	US-10-449-902-19286 Sequence 19286, A

C 26	25.8	14.6	1439	6	US-10-449-902-21106 Sequence 21106, A
C 27	25.8	14.6	4119	7	US-11-217-529-77046 Sequence 77046, A
C 28	25.6	14.5	1775	6	US-10-449-902-81373 Sequence 81373, Ap
C 29	25.6	14.5	2154	6	US-10-449-902-14093 Sequence 14093, A
C 30	25.6	14.5	2627	6	US-10-449-902-21824 Sequence 21824, A
C 31	25.6	14.5	2691	6	US-10-449-902-25676 Sequence 25676, A
C 32	25.6	14.5	3558	7	US-11-131-154-173 Sequence 173, App
C 33	25.4	14.4	1403	7	US-11-313-836-43 Sequence 43, App
C 34	25.4	14.4	1476	7	US-11-217-529-681 Sequence 681, App
C 35	25.4	14.4	1688	6	US-10-953-349-31139 Sequence 31139, A
C 36	25.4	14.4	3016	6	US-10-449-902-12832 Sequence 12832, A
C 37	25.4	14.4	3088	6	US-10-449-902-12783 Sequence 12783, A
C 38	25.2	14.2	1644	6	US-10-449-902-27203 Sequence 27203, A
C 39	25.2	14.2	1773	6	US-10-449-902-475 Sequence 475, App
C 40	25.2	14.2	1782	6	US-10-449-902-22687 Sequence 22687, A
C 41	25.2	14.2	2207	6	US-10-449-902-17975 Sequence 17975, A
C 42	25	14.1	1924	6	US-10-449-902-22070 Sequence 22070, A
C 43	25	14.1	2619	6	US-10-449-902-18809 Sequence 18809, A
C 44	25	14.1	3330	6	US-10-449-902-12737 Sequence 12737, A
C 45	24.8	14.0	937	6	US-10-449-902-1893 Sequence 1893, Ap

ALIGNMENTS

RESULT 1
US-10-449-902-2563/C
Sequence 2563, Application US/10449902
Publication No. US20060123505A1
GENERAL INFORMATION:
APPLICANT: National Institute of Agricultural Sciences.
APPLICANT: Bio-oriented Technology Research Advancement Institution.
APPLICANT: The Institute of Physical and Chemical Research.
APPLICANT: Foundation for Advancement of International Science.
TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
FILE REFERENCE: MOA-A0205Y1-US
CURRENT APPLICATION NUMBER: US/10/449, 902
CURRENT FILING DATE: 2003-05-29
PRIOR APPLICATION NUMBER: JP 2002-203269
PRIOR FILING DATE: 2002-05-30
PRIOR APPLICATION NUMBER: JP 2002-383870
PRIOR FILING DATE: 2002-12-11
NUMBER OF SEQ ID NOS: 56791
SOFTWARE: Patent Ver. 2.1
SEQ ID NO 2563
LENGTH: 1127
TYPE: DNA
ORGANISM: Oryza sativa
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: AK104298
DATABASE ENTRY DATE: 2002-08-28
US-10-449-902-2563

Query Match 17.1%: Score 30.2; DB 6; Length 1127;
Best Local Similarity 53.9%; Pred. No. 0.15; Mismatches 53; Indels 0; Gaps 0;
Matches 62; Conservative 0;

Qy 16 GAGCCAGCTTCTGTGTGCTAACCGCAGCGCAGCACTCTTATCGAAGAGAG 75
Db 199 GCGCGCGGTGTCGCGCATGCGCGCGCGCGCGCGCGCATGACCTCGACAGATCTCTCG 140

Qy 76 CGGCTTCATATCAGCGCGCGCTTATTCATGCGCGTGCAGCGAGAGAGAGAG 130
Db 139 CCCCCGCTCTCTCCGACGCGATCCGACGCGGCGCTCGGTGACGGTGAAGGCC 85

RESULT 2
US-10-449-902-19810/C
Sequence 19810, Application US/10449902
Publication No. US20060123505A1
GENERAL INFORMATION:
APPLICANT: National Institute of Agricultural Sciences.
APPLICANT: Bio-oriented Technology Research Advancement Institution.

APPLICANT: The Institute of Physical and Chemical Research.
APPLICANT: Foundation for Advancement of International Science.
TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
FILE REFERENCE: MOA-A0205Y1-US
CURRENT APPLICATION NUMBER: US/10/449,902
CURRENT FILING DATE: 2003-05-29
PRIOR APPLICATION NUMBER: JP 2002-203269
PRIOR FILING DATE: 2002-05-30
PRIOR APPLICATION NUMBER: JP 2002-383870
PRIOR FILING DATE: 2002-12-11
NUMBER OF SEQ ID NOS: 56791
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 19810
LENGTH: 1128
TYPE: DNA
ORGANISM: *Oryza sativa*
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: AK070153
DATABASE ENTRY DATE: 2001-12-06
US-10-449-902-19810

Query Match 17.1%; Score 30.2; DB 6; Length 1128;
Best Local Similarity 53.9%; Pred. No. 0.15; Indels 0; Gaps 0;
Matches 62; Conservative 0; Mismatches 53; Indels 0; Gaps 0;

QY 16 GAGCGAGCTTCTGTTGCTAACGCGAGCGGCACTCTTATCGGAACAGAGCG 75
DB 200 GCGGCGCGCTGCTCGCCGCACTGCGCGCGCGCGCGCGCGCGCGCGCGCG 141
QY 76 CGCTTCATATCAGCGCGGCTTATCTCATGCGCGTACCGGACAGAGCGCGCC 130
DB 140 CCCCCGCTCTCTCCGACGCGGATCCGAGCGGCGCGCTCGGTACGATGAGGCC 86

RESULT 3
US-10-449-902-22046
Sequence 22046, Application US/10449902
Publication No. US20060123505A1
GENERAL INFORMATION:
APPLICANT: National Institute of Agricultural Sciences.
APPLICANT: Bio-oriented Technology Research Advancement Institution.
APPLICANT: The Institute of Physical and Chemical Research.
APPLICANT: Foundation for Advancement of International Science.
TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
FILE REFERENCE: MOA-A0205Y1-US
CURRENT APPLICATION NUMBER: US/10/449,902
CURRENT FILING DATE: 2003-05-29
PRIOR APPLICATION NUMBER: JP 2002-203269
PRIOR FILING DATE: 2002-05-30
PRIOR APPLICATION NUMBER: JP 2002-383870
PRIOR FILING DATE: 2002-12-11
NUMBER OF SEQ ID NOS: 56791
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 22046
LENGTH: 2019
TYPE: DNA
ORGANISM: *Oryza sativa*
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: AK072256
DATABASE ENTRY DATE: 2001-12-06
US-10-449-902-22046

Query Match 17.1%; Score 30.2; DB 6; Length 2019;
Best Local Similarity 55.1%; Pred. No. 0.18; Indels 48; Gaps 0;
Matches 55; Conservative 0; Mismatches 48; Indels 0; Gaps 0;

QY 38 AACGCGAGCGGAGCACTCTTATCGGAACAGAGCGGCTTATCGGACCGCGCT 97
DB 1562 AACGTCATCAGAGCGGCTCGCTCCCTCCGACGCGGCGCGCGCGCGCGCT 1621
QY 98 TATCTATGCGGCGGACCGGACAGAGCGCGCGCTCCGCTTATCGC 144
DB 1622 GACCTATCGCGGCTGCTCTGTCAGAGGAGCCCAAGAGCGGATCGC 1668

RESULT 4
US-10-449-902-9697
Sequence 9697, Application US/10449902
Publication No. US20060123505A1
GENERAL INFORMATION:
APPLICANT: National Institute of Agricultural Sciences.
APPLICANT: Bio-oriented Technology Research Advancement Institution.
APPLICANT: The Institute of Physical and Chemical Research.
APPLICANT: Foundation for Advancement of International Science.
TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
FILE REFERENCE: MOA-A0205Y1-US
CURRENT APPLICATION NUMBER: US/10/449,902
CURRENT FILING DATE: 2003-05-29
PRIOR APPLICATION NUMBER: JP 2002-203269
PRIOR FILING DATE: 2002-05-30
PRIOR APPLICATION NUMBER: JP 2002-383870
PRIOR FILING DATE: 2002-12-11
NUMBER OF SEQ ID NOS: 56791
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 9697
LENGTH: 2127
TYPE: DNA
ORGANISM: *Oryza sativa*
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: AK107045
DATABASE ENTRY DATE: 2002-08-28
US-10-449-902-9697

Query Match 17.1%; Score 30.2; DB 6; Length 2127;
Best Local Similarity 55.1%; Pred. No. 0.18; Indels 48; Gaps 0;
Matches 59; Conservative 0; Mismatches 48; Indels 0; Gaps 0;

QY 38 AACGCGAGCGGAGCACTCTTATCGGAACAGAGCGGCTTATCGGACCGCGCT 97
DB 1543 AACGTCATCAGAGCGGCTCGCTCCCTCCGACGCGGCGCGCGCGCGCT 1602
QY 98 TATCTATGCGGCGTACCGGACAGAGCGCGCGCTCCGCTTATCGC 144
DB 1603 GACCTATCGCGGCTGCTCTGTCAGAGGAGCCCAAGAGCGGATCGC 1649

RESULT 5
US-10-953-349-32119/C
Sequence 32119, Application US/10953349
Publication No. US20060107345A1
GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nikolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: Patentin Version 3.3
SEQ ID NO 32119
LENGTH: 1114
TYPE: DNA
ORGANISM: *Triticum aestivum*
US-10-953-349-32119

Query Match 16.9%; Score 30; DB 6; Length 1114;
Best Local Similarity 53.4%; Pred. No. 0.17; Indels 55; Gaps 0;
Matches 63; Conservative 0; Mismatches 55; Indels 0; Gaps 0;

QY 29 TGTGTGCTAACGAGCGGAGCACTCTTATCGGAACAGAGCGGCTTATCGA 88
DB 955 TGTGTGCTAACGAGCGGAGCACTCTTATCGGAACAGAGCGGCTTATCGA 896
QY 89 GCGCGGCTTATCTCATGCGCGTACCGGACAGAGCGCGCGCTCCGCTTATCGCGC 146
DB 895 GCGCATGATGCGGTGTTCTGTCGCGGCTCTGACGCGGCGCGGCTCTCCGCGC 838

RESULT 6
US-10-517-441-401/c
; Sequence 401, Application US/10517441
; Publication No. US20060121467A1
; GENERAL INFORMATION:
; APPLICANT: FOCKENS, John
; APPLICANT: HARBECK, Nadia
; APPLICANT: KOENIG, Thomas
; APPLICANT: MAIER, Sabine
; APPLICANT: MARTENS, John
; APPLICANT: MODEL, Fabian
; APPLICANT: NIMBRICH, Inko
; APPLICANT: RUJAN, Tamas
; APPLICANT: SCHMITT, Armin
; APPLICANT: SCHMITT, Manfred
; APPLICANT: LOOK, Maxime P.
; APPLICANT: MARX, Almut
; APPLICANT: HOEFER, Heinz
; TITLE OF INVENTION: Method and nucleic acids for the improved treatment of breast cell
; TITLE OF INVENTION: Proliferative disorders
; FILE REFERENCE: 47675-93
; CURRENT APPLICATION NUMBER: US/10/517,441
; PRIOR FILING DATE: 2004-12-11
; PRIOR APPLICATION NUMBER: PCT/EP2003/010881
; PRIOR FILING DATE: 2003-10-01
; PRIOR APPLICATION NUMBER: DE 10317955.0
; PRIOR FILING DATE: 2003-04-17
; PRIOR APPLICATION NUMBER: DE 10300096.8
; PRIOR FILING DATE: 2003-01-07
; PRIOR APPLICATION NUMBER: DE 10245779.4
; PRIOR FILING DATE: 2002-10-01
; NUMBER OF SEQ ID NOS: 2147
; SEQ ID NO 401
; LENGTH: 3107
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-517-441-401

Query Match 16.9%; Score 30; DB 6; Length 3107;
Best Local Similarity 50.7%; Pred. No. 0.23; Indels 0; Gaps 0;
Matches 72; Conservative 0; Mismatches 70;

QY 6 ATGTGACAGAGCCAGCTTCTGTGTTCTTAACCGAGCGGAGCACTCTATCG 65
DB 2079 AACGGAACACCCCGCTCTCTCGCTTCAACCGCGCGGAAATTAACCTCAACCGCC 2020
QY 66 GAACAGAGCGCGCTCTCATATCAGCGCGGTTATCTCATGCGCGTACCGAGG 125
DB 2019 GAACCGCGAGCTTCTCTCATTTTAAACAATCTTAACGCGCGGAAACGACCGC 1960
QY 126 CGCCCGTCCGCTTATCGGCC 147
DB 1959 CACTTCTCCCATATCGGCC 1938

RESULT 7
US-10-517-441-499/c
; Sequence 499, Application US/10517441
; Publication No. US20060121467A1
; GENERAL INFORMATION:
; APPLICANT: FOCKENS, John
; APPLICANT: HARBECK, Nadia
; APPLICANT: KOENIG, Thomas
; APPLICANT: MAIER, Sabine
; APPLICANT: MARTENS, John
; APPLICANT: MODEL, Fabian
; APPLICANT: NIMBRICH, Inko
; APPLICANT: RUJAN, Tamas
; APPLICANT: SCHMITT, Armin

APPLICANT: SCHMITT, Manfred
APPLICANT: LOOK, Maxime P.
APPLICANT: MARX, Almut
APPLICANT: HOEFER, Heinz
; TITLE OF INVENTION: Method and nucleic acids for the improved treatment of breast cell
; TITLE OF INVENTION: Proliferative disorders
; FILE REFERENCE: 47675-93
; CURRENT APPLICATION NUMBER: US/10/517,441
; PRIOR FILING DATE: 2004-12-11
; PRIOR APPLICATION NUMBER: PCT/EP2003/010881
; PRIOR FILING DATE: 2003-10-01
; PRIOR APPLICATION NUMBER: DE 10317955.0
; PRIOR FILING DATE: 2003-04-17
; PRIOR APPLICATION NUMBER: DE 10300096.8
; PRIOR FILING DATE: 2003-01-07
; PRIOR APPLICATION NUMBER: DE 10245779.4
; PRIOR FILING DATE: 2002-10-01
; NUMBER OF SEQ ID NOS: 2147
; SEQ ID NO 499
; LENGTH: 3501
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-517-441-499

Query Match 16.9%; Score 30; DB 6; Length 3501;
Best Local Similarity 50.7%; Pred. No. 0.24; Indels 0; Gaps 0;
Matches 72; Conservative 0; Mismatches 70;

QY 6 ATGTGACAGAGCCAGCTTCTGTGTTCTTAACCGAGCGGAGCACTCTATCG 65
DB 1585 AACGGAACACCCCGCTCTCTCGCTTCAACCGCGCGGAAATTAACCTCAACCGCC 1526
QY 66 GAACAGAGCGCGCTCTCATATCAGCGCGGTTATCTCATGCGCGTACCGAGG 125
DB 1525 GAACCGCGAGCTTCTCTCATTTTAAACAATCTTAACGCGCGGAAACGACCGC 1466
QY 126 CGCCCGTCCGCTTATCGGCC 147
DB 1465 CACTTCTCCCATATCGGCC 1444

RESULT 8
US-10-449-902-25649
; Sequence 25649, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agricultural Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; PRIOR FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 25649
; LENGTH: 2214
; TYPE: DNA
; ORGANISM: Oryza sativa
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: AK101091
; DATABASE ENTRY DATE: 2002-08-28
US-10-449-902-25649

Query Match 16.7%; Score 29.6; DB 6; Length 2214;
Best Local Similarity 52.4%; Pred. No. 0.29;

	Matches	65;	Conservative	0;	Mismatches	59;	Indels	0;	Gaps	0;
QY	10	TGACAGGAGCGCAGCTTCTGTGTGTGCTTAAACCGGAGCCGGAGCGCAATCTTATGGAAC	69							
Db	78	TGCCAAGAGCGCGCGACCAACCGCGGCGCTCGCGCGCGGTCTCCCGACCGGTCTCCGGGAC	137							
QY	70	AGGAGCGCGCTTCATATCAGCGCGCGGTATCTCATGCGCGTGAACGGACAGAGGCGCG	129							
Db	138	CGGAGGGGAGAGCTCTCCGCGCGCGCGCGGCCCAACAGAGGCGCACTTCAACGCGCTGTCTCA	197							
QY	130	CGTC	133							
Db	198	CGTC	201							

```

RESULT 9
US-10-449-902-24690
: Sequence 24690, Application US/10449902
: Publication NO. US20060123505A1
: GENERAL INFORMATION:
: APPLICANT: National Institute of Agrobiological Sciences.
: APPLICANT: Bio-oriented Technology Research Advancement Institution
: APPLICANT: The Institute of Physical and Chemical Research.
: APPLICANT: Foundation for Advancement of International Science.
: TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
: FILE REFERENCE: MOA-A0205Y1-US
: CURRENT APPLICATION NUMBER: US/10/449,902
: PRIOR FILING DATE: 2003-05-29
: PRIOR APPLICATION NUMBER: JP 2002-203269
: PRIOR FILING DATE: 2002-05-30
: PRIOR APPLICATION NUMBER: JP 2002-383870
: PRIOR FILING DATE: 2002-12-11
: NUMBER OF SEQ ID NOS: 56791
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 24690
: LENGTH: 2586
: TYPE: DNA
: ORGANISM: Oryza sativa
: PUBLICATION INFORMATION:
: DATABASE ACCESSION NUMBER: AK100132
: DATABASE ENTRY DATE: 2002-08-28
US-10-449-902-24690

```

Query Match	16.7%	Score 29.6	DB 6	Length 2586
Best Local Similarity	52.4%	Pred. No. 0.31		
Matches	65	Conservative	0	Mismatches 59
			Indels 0	Gaps 0
QY	10	TGACAGACGCCAGCTTCCTGTGTGCTAACCGACGCCGAGCACTCCTTATCGAAC	69	
Db	66	TGCCAAGAGCGCGGACCAACCGGGGGCGTGGCGCGGCGTCCCAACCGGTTC	125	
QY	70	AGGACGCCCTTCATATACAGCCGCCGCTTATCTCATGCGCTGACCGGACAGAGCGCC	129	
Db	126	CGGAGGGGAGGCTTCGCCGCCGCCGCCGCCCAAGAGGGCGGCACTCAACGGCTGTCTCA	185	
QY	130	CGTC	133	
Db	186	CGTC	189	

```

RESULT 10
US-10-449-902-16689
; Sequence 16689, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29

```

? PRIOR APPLICATION NUMBER: JP 2002-203269
 ? PRIOR FILING DATE: 2002-05-30
 ? PRIOR APPLICATION NUMBER: JP 2002-383870
 ? PRIOR FILING DATE: 2002-12-11
 ? NUMBER OF SEQ ID NOS: 56791
 ? SOFTWARE: PatentIn Ver. 2.1
 ? SEQ ID NO 16689
 ? LENGTH: 2618
 ? TYPE: DNA
 ? ORGANISM: Oryza sativa
 ? PUBLICATION INFORMATION:
 ? DATABASE ACCESSION NUMBER: AK067165
 ? DATABASE ENTRY DATE: 2001-12-06
 US-10-449-902-16689

Query Match	16.7%	Score 29.6	DB 6	Length 2618
Best Local Similarity	52.4%	Pred. No. 0.31	Mismatches 59	Indels 0
Matches	65	Conservative	0	Gaps 0
QY	10	TGACAGAGCGCCAGCTTCTGTGTGCTTACCGGACCGGACGCAACTCTTATCGGAAC	69	
Db	78	TGCCAAGAGGCCGACCAACCGCGGCGCTCGCGCGCGGCTCCCCACCGGTTCCCGGCAC	137	
QY	70	AGGACGCGCCTTCATATATGACCGCGGCTTATCTCATGCGCGGTGACCGGACACAGAGCGCC	129	
Db	138	CGAGGGGGAGACTTCGCGCGCGCGCGGACCCCAACAGAGGCGCACTCAACGCGTGTCA	197	
QY	130	CGTC	133	
Db	198	CGTC	201	

```

RESULT 11
US-10-449-902-14247/c
; Sequence 14247, Application US/10449902
; Publication No. US20060123505A1
GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USBS THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; PRIOR FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14247
; LENGTH: 788
; TYPE: DNA
; ORGANISM: Oryza sativa
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: AK064860
; DATABASE ENTRY DATE: 2001-12-06
US-10-449-902-14247

```

Query Match	15.6%	Score 27.6	DB 6	Length 788
Best Local Similarity	55.1%	Pred. No. 1.1		
Matches	54	Conservative	0	Mismatches 44; Indels 0; Gaps 0
Qy	33	TTGGTAAACCGAGCGGAGCGCAACTCCCTTATCGGAACGAGACGGCGCTTCATATCAGCG	92	
Db	582	TGGGATCCACACCGCTTGATGATTAATCTTATTCGACAGACGAGGCGCCCAATTTGAGAG	523	
Qy	93	CGCGTTATCTCATGCGCGTGAACCGAGACGAGGCGCC	130	
Db	522	TGAGATATAAATGGCCCTGAGCGACGATGATGATACC	485	

Query Match	15.4%	Score 27.2;	DB 6;	Length 2150;
Best Local Similarity	53.8%	Pred. No. 2;		
Matches	56;	Mismatches	48;	Indels 0;
		Conservative		Gaps 0;

RESULT 15
 US-10-449-902-16716
 Sequence 16716, Application US/10449902
 Publication No. US20060123505A1
 GENERAL INFORMATION:
 APPLICANT: National Institute of Agrobiological Sciences.
 APPLICANT: Bio-oriented Technology Research Advancement Institution.
 APPLICANT: The Institute of Physical and Chemical Research.
 APPLICANT: Foundation for Advancement of International Science.
 TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
 FILE REFERENCE: MOA-A0205Y1-US
 CURRENT APPLICATION NUMBER: US/10/449,902
 CURRENT FILING DATE: 2003-05-29
 PRIOR APPLICATION NUMBER: JP 2002-203269
 PRIOR FILING DATE: 2002-05-30
 PRIOR APPLICATION NUMBER: JP 2002-383870
 PRIOR FILING DATE: 2002-12-11
 NUMBER OF SEQ ID NOS: 56791
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 16716
 LENGTH: 1774
 TYPE: DNA

```

; ORGANISM: Oryza sativa
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: AK067192
; DATABASE ENTRY DATE: 2001-12-06
US-10-449-902-16716

```

```

Query Match      15.1%; Score 26.8; DB 6; Length 1774;
Best Local Similarity 64.5%; Pred. No. 2.6;
Matches 40; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

```

```

QY      76 CGCCTCCATATCAAGCCGCGCTTATCTCATGCGCGTACCGGACACGAGGCGCCCGTCCC 135
      70 CGGCTTCGCTCAAGCTTCGCTCTCGCGCGCGCGCGCGGAGCGGAGGACACGCGTGC 129
      136 GC 137
      130 GC 131
Db

```

```

Search completed: June 15, 2006, 18:04:17
Job time : 20.587 secs

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